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**GENE PRODUCTS DIFFERENTIALLY EXPRESSED IN CANCEROUS BREAST
CELLS AND THEIR METHODS OF USE**

STATEMENT OF RIGHTS OF INVENTION

5 The United States Government has certain rights in this invention pursuant to a
CRADA (BG98-053) between Chiron Corporation and the University of California, which
operates the Lawrence Berkeley National Laboratory for the United States Department of
Energy under Contract No. DE-AC03-76SF00098.

10 CROSS-REFERENCING

This patent application claims the benefit of U.S. provisional application serial
number 60/345,637 filed January 8, 2002, which application is incorporated by reference in
its entirety.

15 FIELD OF THE INVENTION

The present invention relates to polynucleotides of human origin in substantially
isolated form and gene products that are differentially expressed in breast cancer cells, and
uses thereof.

20 BACKGROUND OF THE INVENTION

Cancer, like many diseases, is not the result of a single, well-defined cause, but rather
can be viewed as several diseases, each caused by different aberrations in informational
pathways, that ultimately result in apparently similar pathologic phenotypes. Identification
of polynucleotides that correspond to genes that are differentially expressed in cancerous,
25 pre-cancerous, or low metastatic potential cells relative to normal cells of the same tissue
type, provides the basis for diagnostic tools, facilitates drug discovery by providing for
targets for candidate agents, and further serves to identify therapeutic targets for cancer
therapies that are more tailored for the type of cancer to be treated.

Identification of differentially expressed gene products also furthers the
30 understanding of the progression and nature of complex diseases such as cancer, and is key
to identifying the genetic factors that are responsible for the phenotypes associated with
development of, for example, the metastatic phenotype. Identification of gene products that
are differentially expressed at various stages, and in various types of cancers, can both
provide for early diagnostic tests, and further serve as therapeutic targets. Additionally, the

product of a differentially expressed gene can be the basis for screening assays to identify chemotherapeutic agents that modulate its activity (e.g. its expression, biological activity, and the like).

Early disease diagnosis is of central importance to halting disease progression, and reducing morbidity. Analysis of a patient's tumor to identify the gene products that are differentially expressed, and administration of therapeutic agent(s) designed to modulate the activity of those differentially expressed gene products, provides the basis for more specific, rational cancer therapy that may result in diminished adverse side effects relative to conventional therapies. Furthermore, confirmation that a tumor poses less risk to the patient (e.g., that the tumor is benign) can avoid unnecessary therapies. In short, identification of genes and the encoded gene products that are differentially expressed in cancerous cells can provide the basis of therapeutics, diagnostics, prognostics, therametrics, and the like.

Breast cancer is a leading cause of death among women. One of the priorities in breast cancer research is the discovery of new biochemical markers that can be used for diagnosis, prognosis and monitoring of breast cancer. The prognostic usefulness of these markers depends on the ability of the marker to distinguish between patients with breast cancer who require aggressive therapeutic treatment and patients who should be monitored.

While the pathogenesis of breast cancer is unclear, transformation of non-tumorigenic breast epithelium to a malignant phenotype may be the result of genetic factors, especially in women under 30 (Miki, et al., Science, 266: 66-71, 1994). However, it is likely that other, non-genetic factors are also significant in the etiology of the disease. Regardless of its origin, breast cancer morbidity increases significantly if a lesion is not detected early in its progression. Thus, considerable effort has focused on the elucidation of early cellular events surrounding transformation in breast tissue. Such effort has led to the identification of several potential breast cancer markers.

Thus, the identification of new markers associated with breast cancer, and the identification of genes involved in transforming cells into the cancerous phenotype, remains a significant goal in the management of this disease. In exemplary aspects, the invention described herein provides breast cancer diagnostics, prognostics, therametrics, and therapeutics based upon polynucleotides and/or their encoded gene products.

SUMMARY OF THE INVENTION

The present invention provides methods and compositions useful in detection of cancerous cells, identification of agents that modulate the phenotype of cancerous cells, and

identification of therapeutic targets for chemotherapy of cancerous cells. Cancerous breast cells are of particular interest in each of these aspects of the invention. More specifically, the invention provides polynucleotides in substantially isolated form, as well as polypeptides encoded thereby, that are differentially expressed in breast cancer cells. Also provided are
5 antibodies that specifically bind the encoded polypeptides. These polynucleotides, polypeptides and antibodies are thus useful in a variety of diagnostic, therapeutic, and drug discovery methods. In some embodiments, a polynucleotide that is differentially expressed in breast cancer cells can be used in diagnostic assays to detect breast cancer cells. In other
10 embodiments, a polynucleotide that is differentially expressed in breast cancer cells, and/or a polypeptide encoded thereby, is itself a target for therapeutic intervention.

Accordingly, in one aspect the invention provides a method for detecting a cancerous breast cell. In general, the method involves contacting a test sample obtained from a cell that is suspected of being a breast cancer cell with a probe for detecting a gene product
15 differentially expressed in breast cancer. Many embodiments of the invention involve a gene identifiable or comprising a sequence selected from the group consisting of SEQ ID NOS: 1-499, contacting the probe and the gene product for a time sufficient for binding of the probe to the gene product; and comparing a level of binding of the probe to the sample with a level
20 of probe binding to a control sample obtained from a control breast cell of known cancerous state. A modulated (i.e. increased or decreased) level of binding of the probe in the test breast cell sample relative to the level of binding in a control sample is indicative of the cancerous state of the test breast cell. In certain embodiments, the level of binding of the
25 probe in the test cell sample, usually in relation to at least one control gene, is similar to binding of the probe to a cancerous cell sample. In certain other embodiments, the level of binding of the probe in the test cell sample, usually in relation to at least one control gene, is different, i.e. opposite, to binding of the probe to a non-cancerous cell sample. In specific
embodiments, the probe is a polynucleotide probe and the gene product is nucleic acid. In other specific embodiments, the gene product is a polypeptide. In further embodiments, the gene product or the probe is immobilized on an array.

In another aspect, the invention provides a method for assessing the cancerous
30 phenotype (*e.g.*, metastasis, metastatic potential, aberrant cellular proliferation, and the like) of a breast cell comprising detecting expression of a gene product in a test breast cell sample, wherein the gene comprises a sequence selected from the group consisting of SEQ ID NOS: 1-499; and comparing a level of expression of the gene product in the test breast cell sample with a level of expression of the gene in a control cell sample. Comparison of the level of

expression of the gene in the test cell sample relative to the level of expression in the control cell sample is indicative of the cancerous phenotype of the test cell sample. In specific embodiments, detection of gene expression is by detecting a level of an RNA transcript in the test cell sample. In other specific embodiments detection of expression of the gene is by
5 detecting a level of a polypeptide in a test sample.

In another aspect, the invention provides a method for suppressing or inhibiting a cancerous phenotype of a cancerous cell, the method comprising introducing into a mammalian cell an expression modulatory agent (e.g. an antisense molecule, small molecule, antibody, neutralizing antibody, inhibitory RNA molecule, etc.) to inhibition of expression
10 of a gene identified by a sequence selected from the group consisting of SEQ ID NOS: 1-499. Inhibition of expression of the gene inhibits development of a cancerous phenotype in the cell. In specific embodiments, the cancerous phenotype is metastasis, aberrant cellular proliferation relative to a normal cell, or loss of contact inhibition of cell growth. In the context of this invention "expression" of a gene is intended to encompass the expression of
15 an activity of a gene product, and, as such, inhibiting expression of a gene includes inhibiting the activity of a product of the gene.

In another aspect, the invention provides a method for assessing the tumor burden of a subject, the method comprising detecting a level of a differentially expressed gene product in a test sample from a subject suspected of or having a tumor, the differentially expressed
20 gene product comprising a sequence selected from the group consisting of SEQ ID NOS: 1-499. Detection of the level of the gene product in the test sample is indicative of the tumor burden in the subject.

In another aspect, the invention provides a method for identifying a gene product as a target for a cancer therapeutic, the method comprising contacting a cancerous cell expressing
25 a candidate gene product with an anti-cancer agent, wherein the candidate gene product corresponds to a sequence selected from the group consisting of SEQ ID NOS: 1-499; and analyzing the effect of the anti-cancer agent upon a biological activity of the candidate gene product and/or upon a cancerous phenotype of the cancerous cell. Modulation of the biological activity of the candidate gene product and modulation of the cancerous phenotype
30 of the cancerous cell indicates the candidate gene product is a target for a cancer therapeutic. In specific embodiments, the cancerous cell is a cancerous breast cell. In other specific embodiments, the inhibitor is an antisense oligonucleotide. In further embodiments, the cancerous phenotype is aberrant cellular proliferation relative to a normal cell, or colony formation due to loss of contact inhibition of cell growth.

In another aspect, the invention provides a method for identifying agents that modulate (i.e. increase or decrease) the biological activity of a gene product differentially expressed in a cancerous cell, the method comprising contacting a candidate agent with a differentially expressed gene product, the differentially expressed gene product

5 corresponding to a sequence selected from the group consisting of SEQ ID NOS: 1-499; and detecting a modulation in a biological activity of the gene product relative to a level of biological activity of the gene product in the absence of the candidate agent. In specific embodiments, the detecting is by identifying an increase or decrease in expression of the differentially expressed gene product. In other specific embodiments, the gene product is

10 mRNA or cDNA prepared from the mRNA gene product. In further embodiments, the gene product is a polypeptide.

In another aspect, the invention provides a method of inhibiting growth of a tumor cell by modulating expression of a gene product, where the gene product is encoded by a gene identified by a sequence selected from the group consisting of: SEQ ID NOS:1-499.

15 The invention provides a method of determining the cancerous state of a cell, comprising detecting a level of a product of a gene in a test cell wherein said gene is defined by a sequence selected from a group consisting of SEQ ID NOS:1-499 wherein the cancerous state of the test cell is indicated by detection of said level and comparison to a control level of said gene product. In certain embodiments of this method, the gene product

20 is a nucleic acid or a polypeptide. In certain embodiments of this method, the gene product is immobilized on an array. In one embodiment of this method, the control level is a level of said gene product associated with a control cell of known cancerous state. In other embodiments of this method, the known cancerous state is a non-cancerous state. In another embodiment of this method, the level differs from the control level by at least two fold,

25 indicating the test cell is not of the same cancerous state as that indicated by the control level.

The invention also provides a method for detecting a cancerous breast cell in a sample. This method involves detecting a level of a product of a gene in a test sample obtained from a subject wherein said gene is defined by a sequence selected from a group

30 consisting of SEQ ID NOS:1-499, wherein the presence of a cancerous breast cell or metastasized breast cancer cell is indicated by detection of said level and comparison to a control level of said gene product. In certain embodiments of this method, the sample is a sample of breast tissue. In certain other embodiments of this method, the sample is selected from the group consisting of a liver, brain, kidney, lung, bone and skin sample. In one

embodiment of this method, the cancerous breast cell is a metastasized cancerous breast cell. In certain other embodiments of the method, the control level is a level of said gene product associated with a control sample containing cells of known cancerous state. In another embodiment, the known cancerous state is a non-cancerous state.

5 The invention also provides a method for suppressing a cancerous phenotype of a cancerous mammalian cell comprising introducing into said cancerous cell an antisense polynucleotide for inhibition of expression of a gene defined by a sequence selected from the group consisting of SEQ ID NOS: 1-499, wherein inhibition of expression of said gene suppresses development of said cancerous phenotype. In many embodiments of the method,
10 the cancerous phenotype is metastatic. In certain embodiments of the method, the cancerous phenotype is aberrant cellular proliferation relative to a normal cell. In other embodiments of the method, the cancerous phenotype is loss of contact inhibition of cell growth. In certain other embodiments of the method, the cancerous phenotype is aberrant cellular proliferation of a metastasized breast cancer cell relative to a normal cell.

15 The invention further provides a method for assessing the tumor burden of a subject. This method involves detecting a level of a differentially expressed gene product in a test sample from a subject suspected of having a tumor, the differentially expressed gene product comprising a sequence selected from the group consisting of SEQ ID NOS: 1-499; wherein detection of the level of the gene product in the test sample is indicative of the tumor burden
20 in the subject.

 The method further provides a method for identifying a gene product as a target for a cancer therapeutic. This method involves contacting a cancerous cell expressing a candidate gene product with an anti-cancer agent, wherein the candidate gene product corresponds to a sequence selected from the group consisting of SEQ ID NOS: 1-499; and analyzing the
25 effect of the anti-cancer agent upon a biological activity of the candidate gene product and upon a cancerous phenotype of the cancerous cell; wherein modulation of the biological activity of the candidate gene product and modulation of the cancerous phenotype of the cancerous cell indicates the candidate gene product is a target for a cancer therapeutic. In certain embodiments of this method, the cancerous cell is a cancerous breast cell. In other
30 embodiments of this method, the inhibitor is an antisense oligonucleotide. In certain other embodiments of this method, the cancerous phenotype is aberrant cellular proliferation relative to a normal cell. In another embodiment of this method, the cancerous phenotype is colony formation due to loss of contact inhibition of growth.

The invention further provides a method for identifying agents that decrease biological activity of a gene product differentially expressed in a cancerous cell, the method comprising: contacting a candidate agent with a differentially expressed gene product, the differentially expressed gene product corresponding to a sequence selected from the group
5 consisting of SEQ ID NOS: 1-499; and detecting a decrease in a biological activity of the gene product relative to a level of biological activity of the gene product in the absence of the candidate agent. In certain embodiments of this method, the detecting step is by detection of a decrease in expression of the differentially expressed gene product. In certain other
10 embodiments of this method, the gene product is mRNA or a cDNA prepared from the mRNA gene product. In other embodiments of the invention, the gene product is a polypeptide.

The invention further provides a method of inhibiting growth of a tumor cell by modulating expression of a gene product, the gene product being encoded by a gene identified by a sequence selected from the group consisting of: SEQ ID NOS:1-499.

15 These and other objects, advantages, and features of the invention will become apparent to those persons skilled in the art upon reading the details of the invention as more fully described below.

BRIEF DESCRIPTION OF THE FIGURES

20 Fig. 1 is three panels of autoradiographs showing expression of GAK polypeptide in different cell lines.

Fig. 2 is a graph of a hydropathy plot and a table showing the hydrophobic regions of DKFZp566I133.

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Fig. 3 is six panels of photographs of MDA-231 cells exposed to C180-7, C180-8 and positive control antisense (AS) and control (RC) oligonucleotides.

Fig. 4 is an alignment of spot ID 22793 and spot ID 26883.

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Fig. 5 is a figure of three sequence alignments showing the mapping of each of three sequences onto VMP1 (DKFZ).

DETAILED DESCRIPTION OF THE INVENTION

The present invention provides polynucleotides, as well as polypeptides encoded thereby, that are differentially expressed in breast cancer cells. Methods are provided in which these polynucleotides and polypeptides are used for detecting and reducing the growth of breast cancer cells. Also provided are methods in which the polynucleotides and polypeptides of the invention are used in a variety of diagnostic and therapeutic applications for breast cancer.

Before the present invention is described, it is to be understood that this invention is not limited to particular embodiments described, as such may, of course, vary. It is also to be understood that the terminology used herein is for the purpose of describing particular embodiments only, and is not intended to be limiting.

Unless defined otherwise, all technical and scientific terms used herein have the same meaning as commonly understood by one of ordinary skill in the art to which this invention belongs. Although any methods and materials similar or equivalent to those described herein can be used in the practice or testing of the present invention, the preferred methods and materials are now described. All publications and patent applications mentioned herein are incorporated herein by reference to disclose and describe the methods and/or materials in connection with which the publications are cited.

It must be noted that as used herein and in the appended claims, the singular forms "a", "and", and "the" include plural referents unless the context clearly dictates otherwise. Thus, for example, reference to "a polynucleotide" includes a plurality of such polynucleotides and reference to "the breast cancer cell" includes reference to one or more cells and equivalents thereof known to those skilled in the art, and so forth.

The publications and applications discussed herein are provided solely for their disclosure prior to the filing date of the present application. Nothing herein is to be construed as an admission that the present invention is not entitled to antedate such publication by virtue of prior invention. Further, the dates of publication provided may be different from the actual publication dates which may need to be independently confirmed.

Definitions

The terms "polynucleotide" and "nucleic acid", used interchangeably herein, refer to polymeric forms of nucleotides of any length, either ribonucleotides or deoxynucleotides. Thus, these terms include, but are not limited to, single-, double-, or multi-stranded DNA or RNA, genomic DNA, cDNA, DNA-RNA hybrids, or a polymer comprising purine and

pyrimidine bases or other natural, chemically or biochemically modified, non-natural, or derivatized nucleotide bases. These terms further include, but are not limited to, mRNA or cDNA that comprise intronic sequences (see, *e.g.*, Niwa *et al.* (1999) *Cell* 99(7):691-702).

The backbone of the polynucleotide can comprise sugars and phosphate groups (as may typically be found in RNA or DNA), or modified or substituted sugar or phosphate groups.

Alternatively, the backbone of the polynucleotide can comprise a polymer of synthetic subunits such as phosphoramidites and thus can be an oligodeoxynucleoside phosphoramidate or a mixed phosphoramidate-phosphodiester oligomer. Peyrottes *et al.* (1996) *Nucl. Acids Res.* 24:1841-1848; Chaturvedi *et al.* (1996) *Nucl. Acids Res.* 24:2318-

2323. A polynucleotide may comprise modified nucleotides, such as methylated nucleotides and nucleotide analogs, uracyl, other sugars, and linking groups such as fluororibose and thioate, and nucleotide branches. The sequence of nucleotides may be interrupted by non-nucleotide components. A polynucleotide may be further modified after polymerization, such as by conjugation with a labeling component. Other types of modifications included in this definition are caps, substitution of one or more of the naturally occurring nucleotides with an analog, and introduction of means for attaching the polynucleotide to proteins, metal ions, labeling components, other polynucleotides, or a solid support. The term "polynucleotide" also encompasses peptidic nucleic acids (Pooga *et al.* *Curr Cancer Drug Targets.* (2001) 1:231-9).

A "gene product" is a biopolymeric product that is expressed or produced by a gene. A gene product may be, for example, an unspliced RNA, an mRNA, a splice variant mRNA, a polypeptide, a post-translationally modified polypeptide, a splice variant polypeptide etc. Also encompassed by this term is biopolymeric products that are made using an RNA gene product as a template (*i.e.* cDNA of the RNA). A gene product may be made enzymatically, recombinantly, chemically, or within a cell to which the gene is native. In many embodiments, if the gene product is proteinaceous, it exhibits a biological activity. In many embodiments, if the gene product is a nucleic acid, it can be translated into a proteinaceous gene product that exhibits a biological activity.

A composition (*e.g.* a polynucleotide, polypeptide, antibody, or host cell) that is "isolated" or "in substantially isolated form" refers to a composition that is in an environment different from that in which the composition naturally occurs. For example, a polynucleotide that is in substantially isolated form is outside of the host cell in which the polynucleotide naturally occurs, and could be a purified fragment of DNA, could be part of a heterologous vector, or could be contained within a host cell that is not a host cell from

which the polynucleotide naturally occurs. The term "isolated" does not refer to a genomic or cDNA library, whole cell total protein or mRNA preparation, genomic DNA preparation, or an isolated human chromosome. A composition which is in substantially isolated form is usually substantially purified.

5 As used herein, the term "substantially purified" refers to a compound (*e.g.*, a polynucleotide, a polypeptide or an antibody, etc.,) that is removed from its natural environment and is usually at least 60% free, preferably 75% free, and most preferably 90% free from other components with which it is naturally associated. Thus, for example, a composition containing A is "substantially free of" B when at least 85% by weight of the
10 total A+B in the composition is A. Preferably, A comprises at least about 90% by weight of the total of A+B in the composition, more preferably at least about 95% or even 99% by weight. In the case of polynucleotides, "A" and "B" may be two different genes positioned on different chromosomes or adjacently on the same chromosome, or two isolated cDNA species, for example.

15 The terms "polypeptide" and "protein", interchangeably used herein, refer to a polymeric form of amino acids of any length, which can include coded and non-coded amino acids, chemically or biochemically modified or derivatized amino acids, and polypeptides having modified peptide backbones. The term includes fusion proteins, including, but not limited to, fusion proteins with a heterologous amino acid sequence, fusions with
20 heterologous and homologous leader sequences, with or without N-terminal methionine residues; immunologically tagged proteins; and the like.

"Heterologous" refers to materials that are derived from different sources (*e.g.*, from different genes, different species, etc.).

As used herein, the terms "a gene that is differentially expressed in a breast cancer cell," and "a polynucleotide that is differentially expressed in a breast cancer cell" are used
25 interchangeably herein, and generally refer to a polynucleotide that represents or corresponds to a gene that is differentially expressed in a cancerous breast cell when compared with a cell of the same cell type that is not cancerous, *e.g.*, mRNA is found at levels at least about 25%, at least about 50% to about 75%, at least about 90%, at least about 1.5-fold, at least about 2-
30 fold, at least about 5-fold, at least about 10-fold, or at least about 50-fold or more, different (*e.g.*, higher or lower). The comparison can be made in tissue, for example, if one is using in situ hybridization or another assay method that allows some degree of discrimination among cell types in the tissue. The comparison may also or alternatively be made between cells removed from their tissue source.

"Differentially expressed polynucleotide" as used herein refers to a nucleic acid molecule (RNA or DNA) comprising a sequence that represents a differentially expressed gene, *e.g.*, the differentially expressed polynucleotide comprises a sequence (*e.g.*, an open reading frame encoding a gene product; a non-coding sequence) that uniquely identifies a differentially expressed gene so that detection of the differentially expressed polynucleotide in a sample is correlated with the presence of a differentially expressed gene in a sample. "Differentially expressed polynucleotides" is also meant to encompass fragments of the disclosed polynucleotides, *e.g.*, fragments retaining biological activity, as well as nucleic acids homologous, substantially similar, or substantially identical (*e.g.*, having about 90% sequence identity) to the disclosed polynucleotides.

By "cyclin G associated kinase", or "GAK" is meant any polypeptide composition that exhibits cyclin G associated kinase activity. Examples of cyclin G associated kinase include the polypeptide defined by NCBI accession number XM_003450, NM_005255, NP_005246 and NM_031030. Assays for determining whether a polypeptide has cyclin G associated kinase activity are described in Ausubel et al., eds., 1998, Current Protocols in Molecular Biology, John Wiley & Sons, NY. Variants of the human cyclin G associated kinase that retain biological activity may be produced by, *inter alia*, substituting amino acids that are in equivalent positions between two cyclin G associated kinases, such as the cyclin G associated kinases from rat and humans.

With regard to cyclin G associated kinases, further references of interest include: Kanaoka et al, FEBS Lett. 1997 Jan 27;402(1):73-80; Kimura et al, Genomics. 1997 Sep 1;44(2):179-87; Greener et al, J Biol Chem. 2000 Jan 14;275(2):1365-70; and Korolchuk et al, Traffic. 2002 Jun;3(6):428-39.

"DKFZP566I133" and "DKFZ" are used interchangeably herein to refer to a polypeptide composition that exhibits DKFZP566I133 activity. Assays for determining whether a polypeptide has DKFZP566I133 activity (*i.e.* for determining whether DKFZP566I133 may have intracytoplasmatic vacuole promoting activity) are described in Dusetti et al, (Biochem Biophys Res Commun. 2002 Jan 18;290(2):641-9). Variants of the DKFZP566I133 that retain biological activity may be produced by, *inter alia*, substituting amino acids that are in equivalent positions between two DKFZP566I133, such as the DKFZP566I133 from rat and humans. DKFZ is also known as VMP1, or vacuole membrane protein 1.

Alternatively, "DKFZP566I133", or "DKFZ" refers to an amino acid sequence defined by NCBI accession number NP_112200, AAH09758, NM_138839, and

NM_030938, polynucleotides encoding the amino acid sequences set forth in these accession numbers (SEQ ID NO:512 and SEQ ID NO:513, respectively).

In addition, "DKFZP566I133", or "DKFZ" refers to the polynucleotide sequences represented by Spot ID NOS 22793, 26883 and 27450 (SEQ ID NOS: 274-275 and SEQ ID NOS: 276-277 and SEQ ID NOS:459-460, respectively). Figure 4 shows an alignment between Spot ID NOS: 22793, 26883 and VMP1 (NM_030938) (i.e. DKFZ), identifying a VMP1 or DKFZ gene product as corresponding to these spot IDs. Figure 5 depicts fragments of Spot ID NOS 22793, 26883, 27450 which align with VMP1 (SEQ ID NOS 514, 515, and 516 respectively). These fragments, or their encoded products, may also be used as a DKFZ identifying sequence.

"Corresponds to" or "represents" when used in the context of, for example, a polynucleotide or sequence that "corresponds to" or "represents" a gene means that at least a portion of a sequence of the polynucleotide is present in the gene or in the nucleic acid gene product (e.g., mRNA or cDNA). A subject nucleic acid may also be "identified" by a polynucleotide if the polynucleotide corresponds to or represents the gene. Several genes identified by the polynucleotides of the sequence listing may be found in table 1. Genes identified by a polynucleotide may have all or a portion of the identifying sequence wholly present within an exon of a genomic sequence of the gene, or different portions of the sequence of the polynucleotide may be present in different exons (e.g., such that the contiguous polynucleotide sequence is present in an mRNA, either pre- or post-splicing, that is an expression product of the gene). In some embodiments, the polynucleotide may represent or correspond to a gene that is modified in a cancerous cell relative to a normal cell. The gene in the cancerous cell may contain a deletion, insertion, substitution, or translocation relative to the polynucleotide and may have altered regulatory sequences, or may encode a splice variant gene product, for example. The gene in the cancerous cell may be modified by insertion of an endogenous retrovirus, a transposable element, or other naturally occurring or non-naturally occurring nucleic acid. In most cases, a polynucleotide corresponds to or represents a gene if the sequence of the polynucleotide is most identical to the sequence of a gene or its product (e.g. mRNA or cDNA) as compared to other genes or their products. In most embodiments, the most identical gene is determined using a sequence comparison of a polynucleotide to a database of polynucleotides (e.g. GenBank) using the BLAST program at default settings. For example, if the most similar gene in the human genome to an exemplary polynucleotide is the protein kinase C gene, the exemplary polynucleotide corresponds to protein kinase C. In most cases, the sequence of a fragment of

an exemplary polynucleotide is at least 95%, 96%, 97%, 98%, 99% or up to 100% identical to a sequence of at least 15, 20, 25, 30, 35, 40, 45, or 50 contiguous nucleotides of a corresponding gene or its product (mRNA or cDNA), when nucleotides that are "N" represent G, A, T or C.

5 An "identifying sequence" is a minimal fragment of a sequence of contiguous nucleotides that uniquely identifies or defines a polynucleotide sequence or its complement. In many embodiments, a fragment of a polynucleotide uniquely identifies or defines a polynucleotide sequence or its complement. In some embodiments, the entire contiguous sequence of a gene, cDNA, EST, or other provided sequence is an identifying sequence.

10 "Diagnosis" as used herein generally includes determination of a subject's susceptibility to a disease or disorder, determination as to whether a subject is presently affected by a disease or disorder, prognosis of a subject affected by a disease or disorder (*e.g.*, identification of pre-metastatic or metastatic cancerous states, stages of cancer, or responsiveness of cancer to therapy), and use of therametrics (*e.g.*, monitoring a subject's
15 condition to provide information as to the effect or efficacy of therapy).

As used herein, the term "a polypeptide associated with breast cancer" refers to a polypeptide encoded by a polynucleotide that is differentially expressed in a breast cancer cell. Several examples of polypeptides associated with breast cancer are shown in Table 1.

20 The term "biological sample" encompasses a variety of sample types obtained from an organism and can be used in a diagnostic or monitoring assay. The term encompasses blood and other liquid samples of biological origin, solid tissue samples, such as a biopsy specimen or tissue cultures or cells derived therefrom and the progeny thereof. The term encompasses samples that have been manipulated in any way after their procurement, such as by treatment with reagents, solubilization, or enrichment for certain components. The
25 term encompasses a clinical sample, and also includes cells in cell culture, cell supernatants, cell lysates, serum, plasma, biological fluids, and tissue samples.

 The terms "treatment", "treating", "treat" and the like are used herein to generally refer to obtaining a desired pharmacologic and/or physiologic effect. The effect may be prophylactic in terms of completely or partially preventing a disease or symptom thereof
30 and/or may be therapeutic in terms of a partial or complete stabilization or cure for a disease and/or adverse effect attributable to the disease. "Treatment" as used herein covers any treatment of a disease in a mammal, particularly a human, and includes: (a) preventing the disease or symptom from occurring in a subject which may be predisposed to the disease or symptom but has not yet been diagnosed as having it; (b) inhibiting the disease symptom,

i.e., arresting its development; or (c) relieving the disease symptom, i.e., causing regression of the disease or symptom.

The terms "individual," "subject," "host," and "patient," used interchangeably herein and refer to any mammalian subject for whom diagnosis, treatment, or therapy is desired,
5 particularly humans. Other subjects may include cattle, dogs, cats, guinea pigs, rabbits, rats, mice, horses, and the like.

A "host cell", as used herein, refers to a microorganism or a eukaryotic cell or cell line cultured as a unicellular entity which can be, or has been, used as a recipient for a recombinant vector or other transfer polynucleotides, and include the progeny of the original
10 cell which has been transfected. It is understood that the progeny of a single cell may not necessarily be completely identical in morphology or in genomic or total DNA complement as the original parent, due to natural, accidental, or deliberate mutation.

The terms "cancer", "neoplasm", "tumor", and "carcinoma", are used interchangeably herein to refer to cells which exhibit relatively autonomous growth, so that they exhibit an
15 aberrant growth phenotype characterized by a significant loss of control of cell proliferation. In general, cells of interest for detection or treatment in the present application include precancerous (*e.g.*, benign), malignant, pre-metastatic, metastatic, and non-metastatic cells. Detection of cancerous cells is of particular interest.

The term "normal" as used in the context of "normal cell," is meant to refer to a cell
20 of an untransformed phenotype or exhibiting a morphology of a non-transformed cell of the tissue type being examined.

"Cancerous phenotype" generally refers to any of a variety of biological phenomena that are characteristic of a cancerous cell, which phenomena can vary with the type of cancer. The cancerous phenotype is generally identified by abnormalities in, for example,
25 cell growth or proliferation (*e.g.*, uncontrolled growth or proliferation), regulation of the cell cycle, cell mobility, cell-cell interaction, or metastasis, etc.

"Therapeutic target" generally refers to a gene or gene product that, upon modulation of its activity (*e.g.*, by modulation of expression, biological activity, and the like), can provide for modulation of the cancerous phenotype.

30 As used throughout, "modulation" is meant to refer to an increase or a decrease in the indicated phenomenon (*e.g.*, modulation of a biological activity refers to an increase in a biological activity or a decrease in a biological activity).

POLYNUCLEOTIDE COMPOSITIONS

The present invention provides isolated polynucleotides that represent genes that are differentially expressed in breast cancer cells. The polynucleotides, as well as polypeptides encoded thereby, find use in a variety of therapeutic and diagnostic methods.

5 The scope of the invention with respect to compositions containing the isolated polynucleotides useful in the methods described herein includes, but is not necessarily limited to, polynucleotides having a sequence set forth in any one of the polynucleotide sequences provided herein; polynucleotides obtained from the biological materials described herein or other biological sources (particularly human sources) by hybridization under
10 stringent conditions (particularly conditions of high stringency); genes corresponding to the provided polynucleotides; cDNAs corresponding to the provided polynucleotides; variants of the provided polynucleotides and their corresponding genes, particularly those variants that retain a biological activity of the encoded gene product (e.g., a biological activity ascribed to a gene product corresponding to the provided polynucleotides as a result of the assignment
15 of the gene product to a protein family(ies) and/or identification of a functional domain present in the gene product). Other nucleic acid compositions contemplated by and within the scope of the present invention will be readily apparent to one of ordinary skill in the art when provided with the disclosure here. "Polynucleotide" and "nucleic acid" as used herein with reference to nucleic acids of the composition is not intended to be limiting as to the
20 length or structure of the nucleic acid unless specifically indicated.

The invention features polynucleotides that represent genes that are expressed in human tissue, specifically human breast tissue, particularly polynucleotides that are differentially expressed in cancerous breast cells. Nucleic acid compositions described herein of particular interest are at least about 15 bp in length, at least about 30 bp in length,
25 at least about 50 bp in length, at least about 100 bp, at least about 200 bp in length, at least about 300 bp in length, at least about 500 bp in length, at least about 800 bp in length, at least about 1 kb in length, at least about 2.0 kb in length, at least about 3.0 kb in length, at least about 5 kb in length, at least about 10 kb in length, at least about 50kb in length and are usually less than about 200 kb in length. These polynucleotides (or polynucleotide
30 fragments) have uses that include, but are not limited to, diagnostic probes and primers as starting materials for probes and primers, as discussed herein.

The subject polynucleotides usually comprise a sequence set forth in any one of the polynucleotide sequences provided herein, for example, in the sequence listing, incorporated by reference in a table (e.g. by an NCBI accession number), a cDNA deposited at the

A.T.C.C., or a fragment or variant thereof. A "fragment" or "portion" of a polynucleotide is a contiguous sequence of residues at least about 10 nt to about 12 nt, 15 nt, 16 nt, 18 nt or 20 nt in length, usually at least about 22 nt, 24 nt, 25 nt, 30 nt, 40 nt, 50 nt, 60nt, 70 nt, 80 nt, 90 nt, 100 nt to at least about 150 nt, 200 nt, 250 nt, 300 nt, 350 nt, 400 nt, 500 nt, 800 nt or up to about 1000 nt, 1500 or 2000 nt in length. In some embodiments, a fragment of a polynucleotide is the coding sequence of a polynucleotide. A fragment of a polynucleotide may start at position 1 (i.e. the first nucleotide) of a nucleotide sequence provided herein, or may start at about position 10, 20, 30, 50, 75, 100, 150, 200, 250, 300, 350, 400, 450, 500, 600, 700, 800, 900, 1000, 1500 or 2000, or an ATG translational initiation codon of a nucleotide sequence provided herein. In this context "about" includes the particularly recited value or a value larger or smaller by several (5, 4, 3, 2, or 1) nucleotides. The described polynucleotides and fragments thereof find use as hybridization probes, PCR primers, BLAST probes, or as an identifying sequence, for example.

The subject nucleic acids may be variants or degenerate variants of a sequence provided herein. In general, a variants of a polynucleotide provided herein have a fragment of sequence identity that is greater than at least about 65%, greater than at least about 70%, greater than at least about 75%, greater than at least about 80%, greater than at least about 85%, or greater than at least about 90%, 95%, 96%, 97%, 98%, 99% or more (i.e. 100%) as compared to an identically sized fragment of a provided sequence. as determined by the Smith-Waterman homology search algorithm as implemented in MPSRCH program (Oxford Molecular). For the purposes of this invention, a preferred method of calculating percent identity is the Smith-Waterman algorithm. Global DNA sequence identity should be greater than 65% as determined by the Smith-Waterman homology search algorithm as implemented in MPSRCH program (Oxford Molecular) using an gap search with the following search parameters: gap open penalty, 12; and gap extension penalty, 1.

The subject nucleic acid compositions include full-length cDNAs or mRNAs that encompass an identifying sequence of contiguous nucleotides from any one of the polynucleotide sequences provided herein.

As discussed above, the polynucleotides useful in the methods described herein also include polynucleotide variants having sequence similarity or sequence identity. Nucleic acids having sequence similarity are detected by hybridization under low stringency conditions, for example, at 50°C and 10XSSC (0.9 M saline/0.09 M sodium citrate) and remain bound when subjected to washing at 55°C in 1XSSC. Sequence identity can be determined by hybridization under high stringency conditions, for example, at 50°C or

higher and 0.1XSSC (9 mM saline/0.9 mM sodium citrate). Hybridization methods and conditions are well known in the art, see, *e.g.*, USPN 5,707,829. Nucleic acids that are substantially identical to the provided polynucleotide sequences, *e.g.* allelic variants, genetically altered versions of the gene, *etc.*, bind to the provided polynucleotide sequences under stringent hybridization conditions. By using probes, particularly labeled probes of DNA sequences, one can isolate homologous or related genes. The source of homologous genes can be any species, *e.g.* primate species, particularly human; rodents, such as rats and mice; canines, felines, bovines, ovines, equines, yeast, nematodes, *etc.*

In one embodiment, hybridization is performed using a fragment of at least 15 contiguous nucleotides (nt) of at least one of the polynucleotide sequences provided herein. That is, when at least 15 contiguous nt of one of the disclosed polynucleotide sequences is used as a probe, the probe will preferentially hybridize with a nucleic acid comprising the complementary sequence, allowing the identification and retrieval of the nucleic acids that uniquely hybridize to the selected probe. Probes from more than one polynucleotide sequence provided herein can hybridize with the same nucleic acid if the cDNA from which they were derived corresponds to one mRNA.

Polynucleotides contemplated for use in the invention also include those having a sequence of naturally occurring variants of the nucleotide sequences (*e.g.*, degenerate variants (*e.g.*, sequences that encode the same polypeptides but, due to the degenerate nature of the genetic code, different in nucleotide sequence), allelic variants, *etc.*). Variants of the polynucleotides contemplated by the invention are identified by hybridization of putative variants with nucleotide sequences disclosed herein, preferably by hybridization under stringent conditions. For example, by using appropriate wash conditions, variants of the polynucleotides described herein can be identified where the allelic variant exhibits at most about 25-30% base pair (bp) mismatches relative to the selected polynucleotide probe. In general, allelic variants contain 15-25% bp mismatches, and can contain as little as even 5-15%, or 2-5%, or 1-2% bp mismatches, as well as a single bp mismatch.

The invention also encompasses homologs corresponding to any one of the polynucleotide sequences provided herein, where the source of homologous genes can be any mammalian species, *e.g.*, primate species, particularly human; rodents, such as rats; canines, felines, bovines, ovines, equines, yeast, nematodes, *etc.* Between mammalian species, *e.g.*, human and mouse, homologs generally have substantial sequence similarity, *e.g.*, at least 75% sequence identity, usually at least 80%, at least 85, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99% or even 100% identity between

nucleotide sequences. Sequence similarity is calculated based on a reference sequence, which may be a subset of a larger sequence, such as a conserved motif, coding region, flanking region, *etc.* A reference sequence will usually be at least about a fragment of a polynucleotide sequence and may extend to the complete sequence that is being compared.

- 5 Algorithms for sequence analysis are known in the art, such as gapped BLAST, described in Altschul, et al. *Nucleic Acids Res.* (1997) 25:3389-3402, or TeraBLAST available from TimeLogic Corp. (Crystal Bay, Nevada).

Moreover, representative examples of polynucleotide fragments of the invention (useful, for example, as probes), include, for example, fragments comprising, or alternatively
 10 consisting of, a sequence from about nucleotide number 1-50, 51-100, 101-150, 151-200, 201-250, 251-300, 301-350, 351-400, 401-450, 451-500, 501-550, 551-600, 651-700, 701-750, 751-800, 800-850, 851-900, 901-950, 951-1000, 1001-1050, 1051-1100, 1101-1150, 1151-1200, 1201-1250, 1251-1300, 1301-1350, 1351-1400, 1401-1450, 1451-1500, 1501-1550, 1551-1600, 1601-1650, 1651-1700, 1701-1750, 1751-1800, 1801-1850, 1851-1900,
 15 1901-1950, 1951-2000, 2001-2050, 2051-2100, 2101-2150, 2151-2200, 2201-2250, 2251-2300, 2301-2350, 2351-2400, 2401-2450, 2451-2500, 2501-2550, 2551-2600, 2601-2650, 2651-2700, 2701-2750, 2751-2800, 2801-2850, 2851-2900, 2901-2950, 2951-3000, 3001-3050, 3051-3100, 3101-3150, 3151-3200, 3201-3250, 3251-3300, 3301-3350, 3351-3400, 3401-3450, 3451-3500, 3501-3550, 3551-3600, 3601-3650, 3651-3700, 3701-3750, 3751-3800, 3801-3850, 3851-3900, 3901-3950, 3951-4000, 4001-4050, 4051-4100, 4101-4150,
 20 4151-4200, 4201-4250, 4251-4300, 4301-4350, 4351-4400, 4401-4450, 4451-4500, 4501-4550, 4551-4600, 4601-4650, 4651-4700, 4701-4750, 4751-4800, 4801-4850, 4851-4900, 4901-4950, 4951-5000, 5001-5050, 5051-5100, 5101-5150, 5151-5200, 5201-5250, 5251-5300, 5301-5350, 5351-5400, 5401-5450, 5451-5500, 5501-5550, 5551-5600, 5601-5650, 5651-5700, 5701-5750, 5751-5800, 5801-5850, 5851-5900, 5901-5950, 5951-6000, 6001-6050, 6051-6100, 6101-6150, and 6151 of a subject nucleic acid, or the complementary strand thereto. In this context "about" includes the particularly recited range or a range larger or smaller by several (5, 4, 3, 2, or 1) nucleotides, at either terminus or at both termini. In some embodiments, these fragments encode a polypeptide which has a functional activity
 30 (e.g., biological activity) whereas in other embodiments, these fragments are probes, or starting materials for probes. Polynucleotides which hybridize to one or more of these nucleic acid molecules under stringent hybridization conditions or alternatively, under lower stringency conditions, are also encompassed by the invention, as are polypeptides encoded by these polynucleotides or fragments.

The subject nucleic acids can be cDNAs or genomic DNAs, as well as fragments thereof, particularly fragments that encode a biologically active gene product and/or are useful in the methods disclosed herein (e.g., in diagnosis, as a unique identifier of a differentially expressed gene of interest, etc.). The term "cDNA" as used herein is intended to include all nucleic acids that share the arrangement of sequence elements found in native mature mRNA species, where sequence elements are exons and 3' and 5' non-coding regions. Normally mRNA species have contiguous exons, with the intervening introns, when present, being removed by nuclear RNA splicing, to create a continuous open reading frame encoding a polypeptide. mRNA species can also exist with both exons and introns, where the introns may be removed by alternative splicing. Furthermore it should be noted that different species of mRNAs encoded by the same genomic sequence can exist at varying levels in a cell, and detection of these various levels of mRNA species can be indicative of differential expression of the encoded gene product in the cell.

A genomic sequence of interest comprises the nucleic acid present between the initiation codon and the stop codon, as defined in the listed sequences, including all of the introns that are normally present in a native chromosome. It can further include the 3' and 5' untranslated regions found in the mature mRNA. It can further include specific transcriptional and translational regulatory sequences, such as promoters, enhancers, *etc.*, including about 1 kb, but possibly more, of flanking genomic DNA at either the 5' and 3' end of the transcribed region. The genomic DNA can be isolated as a fragment of 100 kbp or smaller; and substantially free of flanking chromosomal sequence. The genomic DNA flanking the coding region, either 3' and 5', or internal regulatory sequences as sometimes found in introns, contains sequences required for proper tissue, stage-specific, or disease-state specific expression.

The nucleic acid compositions of the subject invention can encode all or a part of the naturally-occurring polypeptides. Double or single stranded fragments can be obtained from the DNA sequence by chemically synthesizing oligonucleotides in accordance with conventional methods, by restriction enzyme digestion, by PCR amplification, *etc.*

Probes specific to the polynucleotides described herein can be generated using the polynucleotide sequences disclosed herein. The probes are usually a fragment of a polynucleotide sequences provided herein. The probes can be synthesized chemically or can be generated from longer polynucleotides using restriction enzymes. The probes can be labeled, for example, with a radioactive, biotinylated, or fluorescent tag. Preferably, probes are designed based upon an identifying sequence of any one of the polynucleotide sequences

provided herein. More preferably, probes are designed based on a contiguous sequence of one of the subject polynucleotides that remain unmasked following application of a masking program for masking low complexity (*e.g.*, XBLAST, RepeatMasker, etc.) to the sequence., *i.e.*, one would select an unmasked region, as indicated by the polynucleotides outside the

5 poly-n stretches of the masked sequence produced by the masking program.

The polynucleotides of interest in the subject invention are isolated and obtained in substantial purity, generally as other than an intact chromosome. Usually, the polynucleotides, either as DNA or RNA, will be obtained substantially free of other naturally-occurring nucleic acid sequences that they are usually associated with, generally
10 being at least about 50%, usually at least about 90% pure and are typically "recombinant", *e.g.*, flanked by one or more nucleotides with which it is not normally associated on a naturally occurring chromosome.

The polynucleotides described herein can be provided as a linear molecule or within a circular molecule, and can be provided within autonomously replicating molecules
15 (vectors) or within molecules without replication sequences. Expression of the polynucleotides can be regulated by their own or by other regulatory sequences known in the art. The polynucleotides can be introduced into suitable host cells using a variety of techniques available in the art, such as transferrin polycation-mediated DNA transfer, transfection with naked or encapsulated nucleic acids, liposome-mediated DNA transfer,
20 intracellular transportation of DNA-coated latex beads, protoplast fusion, viral infection, electroporation, gene gun, calcium phosphate-mediated transfection, and the like.

The nucleic acid compositions described herein can be used to, for example, produce polypeptides, as probes for the detection of mRNA in biological samples (*e.g.*, extracts of human cells) or cDNA produced from such samples, to generate additional copies of the
25 polynucleotides, to generate ribozymes or antisense oligonucleotides, and as single stranded DNA probes or as triple-strand forming oligonucleotides. The probes described herein can be used to, for example, determine the presence or absence of any one of the polynucleotide provided herein or variants thereof in a sample. These and other uses are described in more detail below.

30

POLYPEPTIDES AND VARIANTS THEREOF

The present invention further provides polypeptides encoded by polynucleotides that represent genes that are differentially expressed in breast cancer cells. Such polypeptides are referred to herein as "polypeptides associated with breast cancer." The polypeptides can be

used to generate antibodies specific for a polypeptide associated with breast cancer, which antibodies are in turn useful in diagnostic methods, prognostics methods, therametric methods, and the like as discussed in more detail herein. Polypeptides are also useful as targets for therapeutic intervention, as discussed in more detail herein.

5 The polypeptides contemplated by the invention include those encoded by the disclosed polynucleotides and the genes to which these polynucleotides correspond, as well as nucleic acids that, by virtue of the degeneracy of the genetic code, are not identical in sequence to the disclosed polynucleotides. Further polypeptides contemplated by the invention include polypeptides that are encoded by polynucleotides that hybridize to
10 polynucleotide of the sequence listing. Thus, the invention includes within its scope a polypeptide encoded by a polynucleotide having the sequence of any one of the polynucleotide sequences provided herein, or a variant thereof.

 In general, the term "polypeptide" as used herein refers to both the full length polypeptide encoded by the recited polynucleotide, the polypeptide encoded by the gene represented by the recited polynucleotide, as well as portions or fragments thereof.
15 "Polypeptides" also includes variants of the naturally occurring proteins, where such variants are homologous or substantially similar to the naturally occurring protein, and can be of an origin of the same or different species as the naturally occurring protein (*e.g.*, human, murine, or some other species that naturally expresses the recited polypeptide, usually a
20 mammalian species). In general, variant polypeptides have a sequence that has at least about 80%, usually at least about 90%, and more usually at least about 98% sequence identity with a differentially expressed polypeptide described herein, as measured by BLAST 2.0 using the parameters described above. The variant polypeptides can be naturally or non-naturally glycosylated, *i.e.*, the polypeptide has a glycosylation pattern that differs from the
25 glycosylation pattern found in the corresponding naturally occurring protein.

 The invention also encompasses homologs of the disclosed polypeptides (or fragments thereof) where the homologs are isolated from other species, *i.e.* other animal or plant species, where such homologs, usually mammalian species, *e.g.* rodents, such as mice, rats; domestic animals, *e.g.* horse, cow, dog, cat; and humans. By "homolog" is meant a
30 polypeptide having at least about 35%, usually at least about 40% and more usually at least about 60% amino acid sequence identity to a particular differentially expressed protein as identified above, where sequence identity is determined using the BLAST 2.0 algorithm, with the parameters described *supra*.

In general, the polypeptides of interest in the subject invention are provided in a non-naturally occurring environment, *e.g.* are separated from their naturally occurring environment. In certain embodiments, the subject protein is present in a composition that is enriched for the protein as compared to a cell or extract of a cell that naturally produces the protein. As such, isolated polypeptide is provided, where by “isolated” or “in substantially isolated form” is meant that the protein is present in a composition that is substantially free of other polypeptides, where by substantially free is meant that less than 90%, usually less than 60% and more usually less than 50% of the composition is made up of other polypeptides of a cell that the protein is naturally found.

Also within the scope of the invention are variants; variants of polypeptides include mutants, fragments, and fusions. Mutants can include amino acid substitutions, additions or deletions. The amino acid substitutions can be conservative amino acid substitutions or substitutions to eliminate non-essential amino acids, such as to alter a glycosylation site, a phosphorylation site or an acetylation site, or to minimize misfolding by substitution or deletion of one or more cysteine residues that are not necessary for function. Conservative amino acid substitutions are those that preserve the general charge, hydrophobicity/hydrophilicity, and/or steric bulk of the amino acid substituted.

Variants can be designed so as to retain or have enhanced biological activity of a particular region of the protein (*e.g.*, a functional domain and/or, where the polypeptide is a member of a protein family, a region associated with a consensus sequence). For example, muteins can be made which are optimized for increased antigenicity, *i.e.* amino acid variants of a polypeptide may be made that increase the antigenicity of the polypeptide. Selection of amino acid alterations for production of variants can be based upon the accessibility (interior vs. exterior) of the amino acid (*see, e.g., Go et al, Int. J. Peptide Protein Res.* (1980) 15:211), the thermostability of the variant polypeptide (*see, e.g., Querol et al., Prot. Eng.* (1996) 9:265), desired glycosylation sites (*see, e.g., Olsen and Thomsen, J. Gen. Microbiol.* (1991) 137:579), desired disulfide bridges (*see, e.g., Clarke et al., Biochemistry* (1993) 32:4322; and Wakarchuk *et al., Protein Eng.* (1994) 7:1379), desired metal binding sites (*see, e.g., Toma et al., Biochemistry* (1991) 30:97, and Haezebrouck *et al., Protein Eng.* (1993) 6:643), and desired substitutions with in proline loops (*see, e.g., Masul et al., Appl. Env. Microbiol.* (1994) 60:3579). Cysteine-depleted muteins can be produced as disclosed in USPN 4,959,314. Variants also include fragments of the polypeptides disclosed herein, particularly biologically active fragments and/or fragments corresponding to functional domains. Fragments of interest will typically be at least about 10 aa to at least about 15 aa in

length, usually at least about 50 aa in length, and can be as long as 300 aa in length or longer, but will usually not exceed about 1000 aa in length, where the fragment will have a stretch of amino acids that is identical to a polypeptide encoded by a polynucleotide having a sequence of any one of the polynucleotide sequences provided herein, or a homolog thereof.

- 5 The protein variants described herein are encoded by polynucleotides that are within the scope of the invention. The genetic code can be used to select the appropriate codons to construct the corresponding variants.

A fragment of a subject polypeptide is, for example, a polypeptide having an amino acid sequence which is a portion of a subject polypeptide e.g. a polypeptide
10 encoded by a subject polynucleotide that is identified by any one of the sequence of SEQ ID NOS 1 - 499 or its complement. The polypeptide fragments of the invention are preferably at least about 9 aa, at least about 15 aa, and more preferably at least about 20 aa, still more preferably at least about 30 aa, and even more preferably, at least about 40 aa, at least about 50 aa, at least about 75 aa, at least about 100 aa, at least about 125 aa or at least about 150 aa
15 in length. A fragment "at least 20 aa in length," for example, is intended to include 20 or more contiguous amino acids from, for example, the polypeptide encoded by a cDNA, in a cDNA clone contained in a deposited library, or a nucleotide sequence shown in SEQ ID NOS:1-499 or the complementary stand thereof. In this context "about" includes the particularly recited value or a value larger or smaller by several (5, 4, 3, 2, or 1) amino acids.
20 These polypeptide fragments have uses that include, but are not limited to, production of antibodies as discussed herein. Of course, larger fragments (e.g., at least 150, 175, 200, 250, 500, 600, 1000, or 2000 amino acids in length) are also encompassed by the invention.

Moreover, representative examples of polypeptides fragments of the invention (useful in, for example, as antigens for antibody production), include, for example,
25 fragments comprising, or alternatively consisting of, a sequence from about amino acid number 1-10, 5-10, 10-20, 21-31, 31-40, 41-61, 61-81, 91-120, 121-140, 141-162, 162-200, 201-240, 241-280, 281- 320, 321-360, 360-400, 400-450, 451-500, 500-600, 600-700, 700-800, 800-900 and the like. In this context "about" includes the particularly recited range or a range larger or smaller by several (5, 4, 3, 2, or 1) amino acids, at either terminus or at both
30 termini. In some embodiments, these fragments has a functional activity (e.g., biological activity) whereas in other embodiments, these fragments may be used to make an antibody.

Further polypeptide variants may are described in PCT publications WO/00-55173, WO/01-07611 and WO/02-16429

VECTORS, HOST CELLS AND PROTEIN PRODUCTION

The present invention also relates to vectors containing the polynucleotide of the present invention, host cells, and the production of polypeptides by recombinant techniques. The vector may be, for example, a phage, plasmid, viral, or retroviral vector. Retroviral
5 vectors may be replication competent or replication defective. In the latter case, viral propagation generally will occur only in complementing host cells.

The polynucleotides of the invention may be joined to a vector containing a selectable marker for propagation in a host. Generally, a plasmid vector is introduced in a precipitate, such as a calcium phosphate precipitate, or in a complex with a charged lipid. If
10 the vector is a virus, it may be packaged in vitro using an appropriate packaging cell line and then transduced into host cells.

The polynucleotide insert should be operatively linked to an appropriate promoter, such as the phage lambda PL promoter, the E. coli lac, trp, phoA and tac promoters, the SV40 early and late promoters and promoters of retroviral LTRs, to name a few. Other
15 suitable promoters will be known to the skilled artisan. The expression constructs will further contain sites for transcription initiation, termination, and, in the transcribed region, a ribosome binding site for translation. The coding portion of the transcripts expressed by the constructs will preferably include a translation initiating codon at the beginning and a termination codon (UAA, UGA or UAG) appropriately positioned at the end of the
20 polypeptide to be translated.

As indicated, the expression vectors will preferably include at least one selectable marker. Such markers include dihydrofolate reductase, G418 or neomycin resistance for eukaryotic cell culture and tetracycline, kanamycin or ampicillin resistance genes for culturing in E. coli and other bacteria.

25 Representative examples of appropriate hosts include, but are not limited to, bacterial cells, such as E. coli, Streptomyces and Salmonella typhimurium cells; fungal cells, such as yeast cells (e.g., Saccharomyces cerevisiae or Pichia pastoris (ATCC Accession No. 201178)); insect cells such as Drosophila S2 and Spodoptera Sf9 cells; animal cells such as CHO, COS, 293, and Bowes melanoma cells; and plant cells. 5 Appropriate culture mediums
30 and conditions for the above-described host cells are known in the art.

Among vectors preferred for use in bacteria include pQE70, pQE60 and pQE-9, available from QIAGEN, Inc.; pBluescript vectors, Phagescript vectors, pNHSA, pNH16a, pNH18A, pNH46A, available from Stratagene Cloning Systems, Inc.; and ptrc99a, pKK223-3, pKK233-3, pDR540, pRITS available from Pharmacia Biotech, Inc. Among preferred

eukaryotic vectors are pWLNEO, pSV2CAT, pOG44, pXT1 and pSG available from Stratagene; and pSVK3, pBPV, pMSG and pSVL available from Pharmacia. Preferred expression vectors for use in yeast systems include, but are not limited to pYES2, pYDI, pTEFI/Zeo, pYES2/GS, pPICZ, pGAPZ, pGAPZalph, pPIC9, pPIC3.5, pHIL-D2, pHIL-S1, 5 pPIC3.5K, pPIC9K, and PAO815 (all available from Invitrogen, Carload, CA). Other suitable vectors will be readily apparent to the skilled artisan.

Nucleic acids of interest may be cloned into a suitable vector by route methods. Suitable vectors include plasmids, cosmids, recombinant viral vectors e.g. retroviral vectors, YACs, BACs and the like, phage vectors.

10 Introduction of the construct into the host cell can be effected by calcium phosphate transfection, DEAE-dextran mediated transfection, cationic lipid-mediated transfection, electroporation, transduction, infection, or other methods. Such methods are described in many standard laboratory manuals, such as Davis et al., Basic Methods In Molecular Biology (1986). It is specifically contemplated that the polypeptides of the present invention 15 may in fact be expressed by a host cell lacking a recombinant vector.

A polypeptide of this invention can be recovered and purified from recombinant cell cultures by well-known methods including ammonium sulfate or ethanol precipitation, acid extraction, anion or cation exchange chromatography, phosphocellulose chromatography, hydrophobic interaction chromatography, affinity chromatography, hydroxylapatite 20 chromatography and lectin chromatography. Most preferably, high performance liquid chromatography ("HPLC") is employed for purification.

Polypeptides of the present invention can also be recovered from: products purified from natural sources, including bodily fluids, tissues and cells, whether directly isolated or cultured; products of chemical synthetic procedures; and products produced by recombinant 25 techniques from a prokaryotic or eukaryotic host, including, for example, bacterial, yeast higher plant, insect, and mammalian cells. Depending upon the host employed in a recombinant production procedure, the polypeptides of the present invention may be glycosylated or may be non-glycosylated. In addition, polypeptides of the invention may also include an initial modified methionine residue, in some cases as a result of host 30 mediated processes. Thus, it is well known in the art that the N-terminal methionine encoded by the translation initiation codon generally is removed with high efficiency from any protein after translation in all eukaryotic cells. While the N-terminal methionine on most proteins also is efficiently removed in most prokaryotes, for some proteins, this prokaryotic

removal process is inefficient, depending on the nature of the amino acid to which the N-terminal methionine is covalently linked.

Suitable methods and compositions for polypeptide expression may be found in PCT publications WO/00-55173, WO/01-07611 and WO/02-16429.

5 In addition, polypeptides of the invention can be chemically synthesized using techniques known in the art (e.g., see Creighton, 1983, *Proteins: Structures and Molecular Principles*, W.H. Freeman & Co., N.Y., and Hunkapiller et al., *Nature*, 310:105-111 (1984)). For example, a polypeptide corresponding to a fragment of a polypeptide can be synthesized by use of a peptide synthesizer. Furthermore, if desired, nonclassical amino acids or
10 chemical amino acid analogs can be introduced as a substitution or addition into the polypeptide sequence. Non-classical amino acids include, but are not limited to, to the D-isomers of the common amino acids, 2,4-diaminobutyric acid, α -amino isobutyric acid, 4-aminobutyric acid, Abu, 2-amino butyric acid, g-Abu, e-Ahx, 6-amino hexanoic acid, Aib, 2-amino isobutyric acid, 3-amino propionic acid, ornithine, norleucine, norvaline, 5
15 hydroxyproline, sarcosine, citrulline, homocitrulline, cysteic acid, t-butylglycine, t-butylalanine, phenylglycine, cyclohexylalanine, b-alanine, fluoro-amino acids, designer amino acids such as b-methyl amino acids, Ca-methyl amino acids, Na-methyl amino acids, and amino acid analogs in general. Furthermore, the amino acid can be D (dextrorotary) or L (levorotary).

20 Non-naturally occurring variants may be produced using art-known mutagenesis techniques, which include, but are not limited to oligonucleotide mediated mutagenesis, alanine scanning, PCR mutagenesis, site directed mutagenesis (see, e.g., Carter et al., *Nucl. Acids Res.* 73:4331 (1986); and Zoller et al., *Nucl. Acids Res.* 70:6487 (1982)), cassette mutagenesis (see, e.g., Wells et al., *Gene* 34:315 (1985)), restriction selection mutagenesis
25 (see, e.g., Wells et al., *Philos. Trans. R. Soc. London SerA* 377:415 (1986)).

Scanning amino acid analysis can also be employed to identify one or more amino acids along a contiguous sequence. Among the preferred scanning amino acids are relatively small neutral amino acids. Such amino acids include alanine, glycine, serine and cysteine. Alanine is typically a preferred scanning amino acid among this group because it eliminates
30 the side-chain beyond the beta-carbon and is less likely to alter the main-chain conformation of the variant. Alanine is also typically preferred because it is the most common amino acid. If alanine substituting does not yield adequate amounts of variant, an isoteric amino acid can be used.

Any cyseine reside not involved in maintaining the proper conformation of a polypeptide may also be substituted, generally with serine, to improve the oxidative stability of the molecule and prevent aberrant crosslinking. Conversely, cysteine bonds may be added to the polypeptide to improve its stability.

5 The invention additionally, encompasses polypeptides of the present invention which are differentially modified during or after translation, e.g., by glycosylation, acetylation, phosphorylation, amidation, derivatization by known protecting/blocking groups, proteolytic cleavage, linkage to an antibody molecule or other cellular ligand, etc. Any of numerous chemical modifications may be carried out by known techniques, including but not limited,
10 to specific chemical cleavage by cyanogen bromide, trypsin, chymotrypsin, papain, V8 protease, NaBH₄; acetylation, formylation, oxidation, reduction; metabolic synthesis in the presence of tunicamycin; etc.

Additional post-translational modifications encompassed by the invention include, for example, e.g., N-linked or O-linked carbohydrate chains, processing of N-terminal or C-
15 terminal ends), attachment of chemical moieties to the amino acid backbone, chemical modifications of N-linked or O-linked carbohydrate chains, and addition or deletion of an N-terminal methionine residue as a result of procaryotic host cell expression. The polypeptides may also be modified with a detectable label, such as an enzymatic, fluorescent, isotopic or affinity label to allow for detection and isolation of the protein.

20 Also provided by the invention are chemically modified derivatives of the polypeptides of the invention which may provide additional advantages such as increased solubility, stability and circulating time of the polypeptide, or decreased immunogenicity (see U.S. Patent No. 4,179,337). The chemical moieties for derivitization may be selected from water soluble polymers such as polyethylene glycol, ethylene glycol/propylene glycol
25 copolymers, carboxymethylcellulose, dextran, polyvinyl alcohol and the like. The 5 polypeptides may be modified at random positions within the molecule, or at predetermined positions within the molecule and may include one, two, three or more attached chemical moieties.

Suitable methods and compositions for production of modified polypeptides may be
30 found in PCT publications WO/00-55173, WO/01-07611 and WO/02-16429.

ANTIBODIES AND OTHER POLYPEPTIDE OR POLYNUCLEOTIDE BINDING MOLECULES

The present invention further provides antibodies, which may be isolated antibodies, that are specific for a polypeptide encoded by a polynucleotide described herein and/or a

polypeptide of a gene that corresponds to a polynucleotide described herein. Antibodies can be provided in a composition comprising the antibody and a buffer and/or a pharmaceutically acceptable excipient. Antibodies specific for a polypeptide associated with breast cancer are useful in a variety of diagnostic and therapeutic methods, as discussed in detail herein.

Gene products, including polypeptides, mRNA (particularly mRNAs having distinct secondary and/or tertiary structures), cDNA, or complete gene, can be prepared and used for raising antibodies for experimental, diagnostic, and therapeutic purposes. Antibodies may be used to identify a gene corresponding to a polynucleotide. The polynucleotide or related cDNA is expressed as described above, and antibodies are prepared. These antibodies are specific to an epitope on the polypeptide encoded by the polynucleotide, and can precipitate or bind to the corresponding native protein in a cell or tissue preparation or in a cell-free extract of an in vitro expression system.

Antibodies

Further polypeptides of the invention relate to antibodies and T-cell antigen receptors (TCR) which immunospecifically bind a subject polypeptide, subject polypeptide fragment, or variant thereof, and/or an epitope thereof (as determined by immunoassays well known in the art for assaying specific antibody-antigen binding). Antibodies of the invention include, but are not limited to, polyclonal, monoclonal, multispecific, human, humanized or chimeric antibodies, single chain antibodies, Fab fragments, F(ab') fragments, fragments produced by a Fab expression library, anti-idiotypic (anti-Id) antibodies (including, e.g., anti-Id antibodies to antibodies of the invention), and epitope-binding fragments of any of the above. The term "antibody," as used herein, refers to immunoglobulin molecules and immunologically active portions of immunoglobulin molecules, i.e., molecules that contain an antigen binding site that immunospecifically binds an antigen. The immunoglobulin molecules of the invention can be of any type (e.g., IgG, IgE, IgM, IgD, IgA and IgY), class (e.g., IgG1, IgG2, IgG3, IgG4, IgA1 and IgA2) or subclass of immunoglobulin molecule.

Most preferably the antibodies are human antigen-binding antibody fragments of the present invention and include, but are not limited to, Fab, Fab' and F(ab')₂, Fd, single-chain Fvs (scFv), single-chain antibodies, disulfide-linked Fvs (sdFv) and fragments comprising either a V_L or V_H domain. Antigen-binding antibody fragments, including single-chain antibodies, may comprise the variable region(s) alone or in combination with the entirety or a portion of the following: hinge region, C_H1, C_H2, and C_H3 domains. Also included in the

invention are antigen-binding fragments also comprising any combination of variable region(s) with a hinge region, C_H1, C_H2, and C_H3 domains. The antibodies of the invention may be from any animal origin including birds and mammals. Preferably, the antibodies are human, murine (e.g., mouse and rat), donkey, ship rabbit, goat, guinea pig, camel, horse, or chicken.

5 As used herein, "human" antibodies include antibodies having the amino acid sequence of a human immunoglobulin and include antibodies isolated from, human immunoglobulin libraries or from animals transgenic for one or more human immunoglobulin and that do not express endogenous immunoglobulins, as described infra and, for example in, U.S. Patent No. 5,939,598 by Kucherlapati et al.

10 The antibodies of the present invention may be monospecific, bispecific, trispecific or of greater multispecificity. Multispecific antibodies may be specific for different epitopes of a polypeptide of the present invention or may be specific for both a polypeptide of the present invention as well as for a heterologous epitope, such as a heterologous polypeptide or solid support material. See, e.g., PCT publications WO 93/17715; WO 92/08802; WO 91/00360; 15 WO 92/05793; Tutt, et al., J. Immunol. 147:60-69 (1991); U.S. Patent Nos. 4,474,893; 4,714,681; 4,925,648; 5,573,920; 5,601,819; Kostelny et al., J. Immunol. 148:1547-1553 (1992).

Antibodies of the present invention may be described or specified in terms of the epitope(s) or portion(s) of a polypeptide of the present invention which they recognize or 20 specifically bind. The epitope(s) or polypeptide portion(s) may be specified as described herein, e.g., by N-terminal and C-terminal positions, or by size in contiguous amino acid residues. Antibodies which specifically bind any epitope or polypeptide of the present invention may also be excluded. Therefore, the present invention includes antibodies that specifically bind polypeptides of the present invention, and allows for the exclusion of the 25 same.

Antibodies of the present invention may also be described or specified in terms of their cross-reactivity. Antibodies that do not bind any other analog, ortholog, or homolog of a polypeptide of the present invention are included. Antibodies that bind polypeptides with at least 95%, at least 90%, at least 85%, at least 80%, at least 75%, at least 70%, at least 65%, at 30 least 60%, at least 55%, and at least 50% identity (as calculated using methods known in the art and described herein) to a polypeptide of the present invention are also included in the present invention. In specific embodiments, antibodies of the present invention cross-react with murine, rat and/or rabbit homologs of human proteins and the corresponding epitopes thereof. Antibodies that do not bind polypeptides with less than 95%, less than 90%, less than

85%, less than 80%, less than 75%, less than 70%, less than 65%, less than 60%, less than 55%, and less than 50% identity (as calculated using methods known in the art and described herein) to a polypeptide of the present invention are also included in the present invention. In a specific embodiment, the above-described cross-reactivity is with respect to any single specific antigenic or immunogenic polypeptide, or combination(s) of 2, 3, 4, 5, or more of the specific antigenic and/or immunogenic polypeptides disclosed herein. Further included in the present invention are antibodies which bind polypeptides encoded by polynucleotides which hybridize to a polynucleotide of the present invention under stringent hybridization conditions (as described herein). Antibodies of the present invention may also be described or specified in terms of their binding affinity to a polypeptide of the invention. Preferred binding affinities include those with a dissociation constant or K_d less than 5×10^{-2} M, 10^{-2} M, 5×10^{-3} M, 10^{-3} M, 5×10^{-4} M, 10^{-4} M, 5×10^{-5} M, 10^{-5} M, 5×10^{-6} M, 10^{-6} M, 5×10^{-7} M, 10^{-7} M, 5×10^{-8} M, 10^{-8} M, 5×10^{-9} M, 10^{-9} M, 5×10^{-10} M, 10^{-10} M, 5×10^{-11} M, 10^{-11} M, 5×10^{-12} M, 10^{-12} M, 5×10^{-13} M, 10^{-13} M, 5×10^{-14} M, 10^{-14} M, 5×10^{-15} M, or 10^{-15} M.

The invention also provides antibodies that competitively inhibit binding of an antibody to an epitope of the invention as determined by any method known in the art for determining competitive binding, for example, the immunoassays described herein. In preferred embodiments, the antibody competitively inhibits binding to the epitope by at least 95%, at least 90%, at least 85 %, at least 80%, at least 75%, at least 70%, at least 60%, or at least 50%.

Methods for making screening, humanizing, and modifying different types of antibody are well known in the art and may be found in PCT publications WO/00-55173, WO/01-07611 and WO/02-16429.

Antibodies of the present invention may act as agonists or antagonists of the polypeptides of the present invention. For example, the present invention includes antibodies which disrupt the receptor/ligand interactions with the polypeptides of the invention either partially or fully. Preferably, antibodies of the present invention bind an antigenic epitope disclosed herein, or a portion thereof. The invention features both receptor-specific antibodies and ligand-specific antibodies. The invention also features receptor-specific antibodies which do not prevent ligand binding but prevent receptor activation. Receptor activation (i.e., signaling) may be determined by techniques described herein or otherwise known in the art. For example, receptor activation can be determined by detecting the phosphorylation (e.g., tyrosine or serine/threonine) of the receptor or its substrate by immunoprecipitation followed by western blot analysis (for example, as described supra). In specific embodiments, antibodies are provided

that inhibit ligand activity or receptor activity by at least 95%, at least 90%, at least 85%, at least 80%, at least 75%, at least 70%, at least 60%, or at least 50% of the activity in absence of the antibody.

The invention also features receptor-specific antibodies which both prevent ligand
5 binding and receptor activation as well as antibodies that recognize the receptor-ligand complex, and, preferably, do not specifically recognize the unbound receptor or the unbound ligand. Likewise, included in the invention are neutralizing antibodies which bind the ligand and prevent binding of the ligand to the receptor, as well as antibodies which bind the ligand, thereby preventing receptor activation, but do not prevent the ligand from binding the receptor.
10 Further included in the invention are antibodies which activate the receptor. These antibodies may act as receptor agonists, i.e., potentiate or activate either all or a subset of the biological activities of the ligand-mediated receptor activation, for example, by inducing dimerization of the receptor. The antibodies may be specified as agonists, antagonists or inverse agonists for biological activities comprising the specific biological activities of the peptides of the invention
15 disclosed herein. The above antibody agonists can be made using methods known in the art. See, e.g., PCT publication WO 96/40281; U.S. Patent No. 5,811,097; Deng et al., Blood 92(6): 1981-1988 (1998); Chen et al., Cancer Res. 58(16):3668-4998 (1998); Harrop et al., J. Immunol. 161(4): 1786-1794 (1998); Zhu et al., Cancer Res. 58(15):3209-3214 (1998); Yoon et al., J. Immunol. 160(7):3170-3179 (1998); Prat et al., J. Cell. Sci. 111(Pt2):237-247 (1998);
20 Pitard et al., J. Immunol. Methods 205(2): 177-190 (1997); Liautard et al., Cytokine 9(4):233-241 (1997); Carlson et al., J. Biol. Chem. 272(17): 11295-11301 (1997); Taryman et al., Neuron 14(4):755-762 (1995); Muller et al., Structure 6(9): 1153-1167 (1998); Bartunek et al., Cytokine 8(1):14-20 (1996) (which are all incorporated by reference herein in their entireties).

Antibodies of the present invention may be used, for example, but not limited to, to
25 purify, detect, and target the polypeptides of the present invention, including both in vitro and in vivo diagnostic and therapeutic methods. For example, the antibodies have use in immunoassays for qualitatively and quantitatively measuring levels of the polypeptides of the present invention in biological samples. See, e.g., Harlow et al., Antibodies: A Laboratory Manual, (Cold Spring Harbor Laboratory Press, 2nd ed. 1988) (incorporated by reference herein in its entirety).

30 Further methods and compositions involving antibodies may be found in PCT publications WO/00-55173, WO/01-07611 and WO/02-16429.

Polynucleotides Encoding Antibodies

The invention further provides polynucleotides comprising a nucleotide sequence encoding an antibody of the invention and fragments thereof. The invention also

encompasses polynucleotides that hybridize under stringent or alternatively, under lower stringency hybridization conditions, e.g., as defined supra, to polynucleotides that encode an antibody, preferably, that specifically binds to a polypeptide of the invention, preferably, an antibody that binds to a subject polypeptide.

5 The polynucleotides may be obtained, and the nucleotide sequence of the polynucleotides determined, by any method known in the art. For example, if the nucleotide sequence of the antibody is known, a polynucleotide encoding the antibody may be assembled from chemically synthesized oligonucleotides (e.g., as described in Kutmeier et al., BioTechniques 17:242 (1994)). which, briefly, involves the synthesis of overlapping
10 oligonucleotides containing portions of the sequence encoding the antibody, annealing and ligating of those oligonucleotides, and then amplification of the ligated oligonucleotides by PCR.

 Alternatively, a polynucleotide encoding an antibody may be generated from nucleic acid from a suitable source. If a clone containing a nucleic acid encoding a particular antibody is not available, but the sequence of the antibody molecule is known, a nucleic acid encoding the
15 immunoglobulin may be chemically synthesized or obtained from a suitable source (e.g., an antibody cDNA library, or a cDNA library generated from, or nucleic acid, preferably poly A+ RNA, isolated from, any tissue or cells expressing the antibody, such as hybridoma cells selected to express an antibody of the invention) by PCR amplification using synthetic primers hybridizable to the 3' and 5' ends of the sequence or by cloning using an oligonucleotide probe
20 specific for the particular gene sequence to identify, e.g., a cDNA clone from a cDNA library that encodes the antibody. Amplified nucleic acids generated by ' PCR may then be cloned into replicable cloning vectors using any method well known in the art.

 Once the nucleotide sequence and corresponding amino acid sequence of the antibody is determined, the nucleotide sequence of the antibody may be manipulated using methods well
25 known in the art for the manipulation of nucleotide sequences, e.g., recombinant DNA techniques, site directed mutagenesis, PCR, etc. (see, for example, the techniques described in Sambrook et al., 1990, Molecular Cloning, A Laboratory Manual, 2d Ed., Cold Spring Harbor Laboratory, Cold Spring Harbor, NY and Ausubel et al., eds., 1998, Current Protocols in Molecular Biology, John Wiley & Sons, NY, which are both incorporated by reference herein in their entireties), to
30 generate antibodies having a different amino acid sequence, for example to create amino acid substitutions, deletions, and/or insertions.

Methods of Producing Antibodies

 The antibodies of the invention can be produced by any method known in the art for the synthesis of antibodies, in particular, by chemical synthesis or preferably, by recombinant

expression techniques. Recombinant expression of an antibody of the invention, or fragment, derivative or analog thereof, (e.g., a heavy or light chain of an antibody of the invention or a single chain antibody of the invention), requires construction of an expression vector containing a polynucleotide that encodes the antibody. Once a polynucleotide encoding an antibody molecule
5 or a heavy or light chain of an antibody, or portion thereof (preferably containing the heavy or light chain variable domain), of the invention has been obtained, the vector for the production of the antibody molecule may be produced by recombinant DNA technology using techniques well known in the art. Thus, methods for preparing a protein by expressing a polynucleotide containing an antibody encoding nucleotide sequence are described herein. Methods which are well known to
10 those skilled in the art can be used to construct expression vectors containing antibody coding sequences and appropriate transcriptional and translational control signals. These methods include, for example, in vitro recombinant DNA techniques, synthetic techniques, and in vivo genetic recombination. The invention, thus, provides replicable vectors comprising a nucleotide sequence encoding an antibody molecule of the invention, or a heavy or light chain thereof, or a
15 heavy or light chain variable domain, operably linked to a promoter. Such vectors may include the nucleotide sequence encoding the constant region of the antibody molecule (see, e.g., PCT Publication WO 86/05807; PCT Publication WO 89/01036; and U.S. Patent No. 5,122,464) and the variable domain of the antibody may be cloned into such a vector for expression of the entire heavy or light chain.

20 The expression vector is transferred to a host cell by conventional techniques and the transfected cells are then cultured by conventional techniques to produce an antibody of the invention. Thus, the invention includes host cells containing a polynucleotide encoding an antibody of the invention, or a heavy or light chain thereof, or a single chain antibody of the invention, operably linked to a heterologous promoter. In preferred embodiments for the
25 expression of double-chained antibodies, vectors encoding both the heavy and light chains may be co-expressed in the host cell for expression of the entire immunoglobulin molecule, as detailed below.

A variety of host-expression vector systems may be utilized to express the antibody molecules of the invention. Such host-expression systems represent vehicles by which the coding
30 sequences of interest may be produced and subsequently purified, but also represent cells which may, when transformed or transfected with the appropriate nucleotide coding sequences, express an antibody molecule of the invention in situ. These include but are not limited to microorganisms such as bacteria (e.g., *E. coli*, *B. subtilis*) transformed with recombinant bacteriophage DNA, plasmid DNA or cosmid DNA expression vectors containing antibody

coding sequences; yeast (e.g., *Saccharomyces*, *Pichia*) transformed with recombinant yeast expression vectors containing antibody coding sequences; insect cell systems infected with recombinant virus expression vectors (e.g., baculovirus) containing antibody coding sequences; plant cell systems infected with recombinant virus expression vectors (e.g., cauliflower mosaic virus, CaMV; tobacco mosaic virus, TMV) or transformed with recombinant plasmid expression vectors (e.g., Ti plasmid) containing antibody coding sequences; or mammalian cell systems (e.g., COS, CHO, BHK, 293, 3T3 cells) harboring recombinant expression constructs containing promoters derived from the genome of mammalian cells (e.g., metallothionein promoter) or from mammalian viruses (e.g., the adenovirus late promoter; the vaccinia virus 7.5K promoter). Preferably, bacterial cells such as *Escherichia coli*, and more preferably, eukaryotic cells, especially for the expression of whole recombinant antibody molecule, are used for the expression of a recombinant antibody molecule. For example, mammalian cells such as Chinese hamster ovary cells (CHO), in conjunction with a vector such as the major intermediate early gene promoter element from human cytomegalovirus is an effective expression system for antibodies (Foecking et al., Gene 45:101 (1986); Cockett et al., *Bio/Technology* 8:2 (1990)).

In bacterial systems, a number of expression vectors may be advantageously selected depending upon the use intended for the antibody molecule being expressed. For example, when a large quantity of such a protein is to be produced, for the generation of pharmaceutical compositions of an antibody molecule, vectors which direct the expression of high levels of fusion protein products that are readily purified may be desirable. Such vectors include, but are not limited, to the *E. coli* expression vector pUR278 (Ruther et al., *EMBO J.* 2:1791 (1983)), in which the antibody coding sequence may be ligated individually into the vector in frame with the lac Z coding region so that a fusion protein is produced; pIN vectors (Inouye & Inouye, *Nucleic Acids Res.* 13:3101-3109 (1985); Van Heeke & Schuster, *J. Biol. Chem.* 24:5503-5509 (1989)); and the like. pGEX vectors may also be used to express foreign polypeptides as fusion proteins with glutathione S-transferase (GST). In general, such fusion proteins are soluble and can easily be purified from lysed cells by adsorption and binding to matrix glutathione-agarose beads followed by elution in the presence of free glutathione. The pGEX vectors are designed to include thrombin or factor Xa protease cleavage sites so that the cloned target gene product can be released from the GST moiety.

In an insect system, *Autographa californica* nuclear polyhedrosis virus (AcNPV) is used as a vector to express foreign genes. The virus grows in *Spodoptera frugiperda* cells. The antibody coding sequence may be cloned individually into non-essential regions (for

example the polyhedrin gene) of the virus and placed under control of an AcNPV promoter (for example the polyhedrin promoter).

In mammalian host cells, a number of viral-based expression systems may be utilized. In cases where an adenovirus is used as an expression vector, the antibody coding sequence of interest may be ligated to an adenovirus transcription/translation control complex, e.g., the late promoter and tripartite leader sequence. This chimeric gene may then be inserted in the adenovirus genome by in vitro or in vivo recombination. Insertion in a non-essential region of the viral genome (e.g., region E1 or E3) will result in a recombinant virus that is viable and capable of expressing the antibody molecule in infected hosts, (e.g., see Logan & Shenk, Proc. Natl. Acad. Sci. USA 81:355-359 (1984)). Specific initiation signals may also be required for efficient translation of inserted antibody coding sequences. These signals include the ATG initiation codon and adjacent sequences. Furthermore, the initiation codon must be in phase with the reading frame of the desired coding sequence to ensure translation of the entire insert. These exogenous translational control signals and initiation codons can be of a variety of origins, both natural and synthetic. The efficiency of expression may be enhanced by the inclusion of appropriate transcription enhancer elements, transcription terminators, etc. (see Bittner et al., Methods in Enzymol. 153:51-544 (1987)).

Antibodies production is well known in the art. Exemplary methods and compositions for making antibodies may be found in PCT publications WO/00-55173, WO/01-07611 and WO/02-16429.

Immunophenotyping

The antibodies of the invention may be utilized for immunophenotyping of cell lines and biological samples. The translation product of the gene of the present invention may be useful as a cell specific marker, or more specifically as a cellular marker that is differentially expressed at various stages of differentiation and/or maturation of particular cell types. Monoclonal antibodies directed against a specific epitope, or combination of epitopes, will allow for the screening of cellular populations expressing the marker. Various techniques can be utilized using monoclonal antibodies to screen for cellular populations expressing the marker(s), and include magnetic separation using antibody-coated magnetic beads, "panning" with antibody attached to a solid matrix (i.e., plate), and flow cytometry (See, e.g., U.S. Patent 5,985,660; and Morrison *et al. Cell*, 96:737-49 (1999)).

These techniques allow for the screening of particular populations of cells, such as might be found with hematological malignancies (i.e. minimal residual disease (MRD) in acute leukemic patients) and "non-self cells in transplantations to prevent Graft-versus-Host

Disease (GVHD). Alternatively, these techniques allow for the screening of hematopoietic stem and progenitor cells capable of undergoing proliferation and/or differentiation, as might be found in human umbilical cord blood.

Assays For Antibody Binding

5 The antibodies of the invention may be assayed for immunospecific binding by any method known in the art. The immunoassays which can be used include but are not limited to competitive and non-competitive assay systems using techniques such as western blots, radioimmunoassays, ELISA (enzyme linked immunosorbent assay), "sandwich" immunoassays, immunoprecipitation assays, precipitin reactions, gel diffusion precipitin
10 reactions, immunodiffusion assays, agglutination assays, complement-fixation assays, immunoradiometric assays, fluorescent immunoassays, protein A immunoassays, to name but a few. Such assays are routine and well known in the art (see, e.g., Ausubel et al, eds, 1994, Current Protocols in Molecular Biology, Vol. 1, John Wiley & Sons, Inc., New York, which is incorporated by reference herein in its entirety). Exemplary immunoassays are described briefly
15 below (but are not intended by way of limitation).

Immunoprecipitation protocols generally comprise lysing a population of cells in a lysis buffer such as RIPA buffer (1% NP-40 or Triton X- 100, 1% sodium deoxycholate, 0.1% SDS, 0.15 M NaCl, 0.01 M sodium phosphate at pH 7.2, 1% Trasylol) supplemented with protein phosphatase and/or protease inhibitors (e.g., EDTA, PMSF, aprotinin, sodium vanadate), adding
20 the antibody of interest to the cell lysate, incubating for a period of time (e.g., 1-4 hours) at 4° C, adding protein A and/or protein G sepharose beads to the cell lysate, incubating for about an hour or more at 4° C, washing the beads in lysis buffer and resuspending the beads in SDS/sample buffer. The ability of the antibody of interest to immunoprecipitate a particular antigen can be assessed by, e.g., western blot analysis. One of skill in the art would be knowledgeable as to the
25 parameters that can be modified to increase the binding of the antibody to an antigen and decrease the background (e.g., pre-clearing the cell lysate with sepharose beads). For further discussion regarding immunoprecipitation protocols see, e.g., Ausubel et al, eds, 1994, Current Protocols in Molecular Biology, Vol. 1, John Wiley & Sons, Inc., New York at 10.16.1.

Western blot analysis generally comprises preparing protein samples, electrophoresis of the
30 protein samples in a polyacrylamide gel (e.g., 8%- 20% SDS-PAGE depending on the molecular weight of the antigen), transferring the protein sample from the polyacrylamide gel to a membrane such as nitrocellulose, PVDF or nylon, blocking the membrane in blocking solution (e.g., PBS with 3% BSA or non-fat milk), washing the membrane in washing buffer (e.g., PBS-Tween 20), blocking the membrane with primary antibody (the antibody of interest) diluted in blocking

buffer, washing the membrane in washing buffer, blocking the membrane with a secondary antibody (which recognizes the primary antibody, e.g., an anti-human antibody) conjugated to an enzymatic substrate (e.g., horseradish peroxidase or alkaline phosphatase) or radioactive molecule (e.g., ³²P or ¹²⁵I) diluted in blocking buffer, washing the membrane in wash buffer, and detecting the presence of the antigen. One of skill in the art would be knowledgeable as to the parameters that can be modified to increase the signal detected and to reduce the background noise. For further discussion regarding western blot protocols see, e.g., Ausubel et al, eds, 1994, Current Protocols in Molecular Biology, Vol. 1, John Wiley & Sons, Inc., New York at 10.8.1.

ELISAs comprise preparing antigen, coating the well of a 96 well microtiter plate with the antigen, adding the antibody of interest conjugated to a detectable compound such as an enzymatic substrate (e.g., horseradish peroxidase or alkaline phosphatase) to the well and incubating for a period of time, and detecting the presence of the antigen. In ELISAs the antibody of interest does not have to be conjugated to a detectable compound; instead, a second antibody (which recognizes the antibody of interest) conjugated to a detectable compound may be added to the well. Further, instead of coating the well with the antigen, the antibody may be coated to the well. In this case, a second antibody conjugated to a detectable compound may be added following the addition of the antigen of interest to the coated well. One of skill in the art would be knowledgeable as to the parameters that can be modified to increase the signal detected as well as other variations of ELISAs known in the art. For further discussion regarding ELISAs see, e.g., Ausubel et al, eds, 1994, Current Protocols in Molecular Biology, Vol. 1, John Wiley & Sons, Inc., New York at 11.2.1.

The binding affinity of an antibody to an antigen and the off-rate of an antibody-antigen interaction can be determined by competitive binding assays. One example of a competitive binding assay is a radioimmunoassay comprising the incubation of labeled antigen (e.g., ³H or ¹²⁵I) with the antibody of interest in the presence of increasing amounts of unlabeled antigen, and the detection of the antibody bound to the labeled antigen. The affinity of the antibody of interest for a particular antigen and the binding off-rates can be determined from the data by scatchard plot analysis. Competition with a second antibody can also be determined using radioimmunoassays. In this case, the antigen is incubated with antibody of interest conjugated to a labeled compound (e.g., ³H or ¹²⁵I) in the presence of increasing amounts of an unlabeled second antibody.

Therapeutic Uses

The present invention is further directed to antibody-based therapies which involve administering antibodies of the invention to an animal, preferably a mammal, and most

preferably a human, patient for treating one or more of the disclosed diseases, disorders, or conditions. Therapeutic compounds of the invention include, but are not limited to, antibodies of the invention (including fragments, analogs and derivatives thereof as described herein) and nucleic acids encoding antibodies of the invention (including fragments, analogs and derivatives thereof and anti-idiotypic antibodies as described herein). The antibodies of the invention can be used to treat, inhibit or prevent diseases, disorders or conditions associated with aberrant expression and/or activity of a polypeptide of the invention, including, but not limited to, any one or more of the diseases, disorders, or conditions described herein. The treatment and/or prevention of diseases, disorders, or conditions associated with aberrant expression and/or activity of a polypeptide of the invention includes, but is not limited to, alleviating symptoms associated with those diseases, disorders or conditions. Antibodies of the invention may be provided in pharmaceutically acceptable compositions as known in the art or as described herein.

A summary of the ways in which the antibodies of the present invention may be used therapeutically includes binding polynucleotides or polypeptides of the present invention locally or systemically in the body or by direct cytotoxicity of the antibody, e.g. as mediated by complement (CDC) or by effector cells (ADCC). Some of these approaches are described in more detail below. Armed with the teachings provided herein, one of ordinary skill in the art will know how to use the antibodies of the present invention for diagnostic, monitoring or therapeutic purposes without undue experimentation.

The antibodies of this invention may be advantageously utilized in combination with other monoclonal or chimeric antibodies, or with lymphokines or hematopoietic growth factors (such as, e.g., IL-2, IL-3 and IL-7), for example, which serve to increase the number or activity of effector cells which interact with the antibodies.

The antibodies of the invention may be administered alone or in combination with other types of treatments (e.g., radiation therapy, chemotherapy, hormonal therapy, immunotherapy and anti-tumor agents). Generally, administration of products of a species origin or species reactivity (in the case of antibodies) that is the same species as that of the patient is preferred. Thus, in a preferred embodiment, human antibodies, fragments derivatives, analogs, or nucleic acids, are administered to a human patient for therapy or prophylaxis.

It is preferred to use high affinity and/or potent in vivo inhibiting and/or neutralizing antibodies against polypeptides or polynucleotides of the present invention, fragments or regions thereof, for both immunoassays directed to and therapy of disorders related to polynucleotides or polypeptides, including fragments thereof, of the present invention. Such antibodies, fragments, or regions, will preferably have an affinity for polynucleotides or

polypeptides of the invention, including fragments thereof. Preferred binding affinities include those with a dissociation constant or K_d less than 5×10^{-2} M, 10^{-2} M, 5×10^{-3} M, 10^{-3} M, 5×10^{-4} M, 10^{-4} M, 5×10^{-5} M, 10^{-5} M, 5×10^{-6} M, 10^{-6} M, 5×10^{-7} M, 10^{-7} M, 5×10^{-8} M, 10^{-8} M, 5×10^{-9} M, 10^{-9} M, 5×10^{-10} M, 10^{-10} M, 5×10^{-11} M, 10^{-11} M, 5×10^{-12} M, 10^{-12} M, 5×10^{-13} M, 10^{-13} M, 5×10^{-14} M, 10^{-14} M, 5×10^{-15} M, or 10^{-15} M.

KITS

Also provided by the subject invention are kits for practicing the subject methods, as described above. The subject kits include at least one or more of: a subject nucleic acid, isolated polypeptide or an antibody thereto. Other optional components of the kit include: restriction enzymes, control primers and plasmids; buffers, cells, carriers adjuvants etc. The nucleic acids of the kit may also have restriction sites, multiple cloning sites, primer sites, etc to facilitate their ligation other plasmids. The various components of the kit may be present in separate containers or certain compatible components may be precombined into a single container, as desired. In many embodiments, kits with unit doses of the active agent, e.g. in oral or injectable doses, are provided. In certain embodiments, controls, such as samples from a cancerous or non-cancerous cell are provided by the invention. Further embodiments of the kit include an antibody for a subject polypeptide and a chemotherapeutic agent to be used in combination with the polypeptide as a treatment.

In addition to above-mentioned components, the subject kits typically further include instructions for using the components of the kit to practice the subject methods. The instructions for practicing the subject methods are generally recorded on a suitable recording medium. For example, the instructions may be printed on a substrate, such as paper or plastic, etc. As such, the instructions may be present in the kits as a package insert, in the labeling of the container of the kit or components thereof (i.e., associated with the packaging or subpackaging) etc. In other embodiments, the instructions are present as an electronic storage data file present on a suitable computer readable storage medium, e.g. CD-ROM, diskette, etc. In yet other embodiments, the actual instructions are not present in the kit, but means for obtaining the instructions from a remote source, e.g. via the internet, are provided. An example of this embodiment is a kit that includes a web address where the instructions can be viewed and/or from which the instructions can be downloaded. As with the instructions, this means for obtaining the instructions is recorded on a suitable substrate.

COMPUTER-RELATED EMBODIMENTS

In general, a library of polynucleotides is a collection of sequence information, which information is provided in either biochemical form (*e.g.*, as a collection of polynucleotide molecules), or in electronic form (*e.g.*, as a collection of polynucleotide sequences stored in a computer-readable form, as in a computer system and/or as part of a computer program).
5 The sequence information of the polynucleotides can be used in a variety of ways, *e.g.*, as a resource for gene discovery, as a representation of sequences expressed in a selected cell type (*e.g.*, cell type markers), and/or as markers of a given disease or disease state. For example, in the instant case, the sequences of polynucleotides and polypeptides
10 corresponding to genes differentially expressed in cancer, particular in breast cancer, as well as the nucleic acid and amino acid sequences of the genes themselves, can be provided in electronic form in a computer database.

In general, a disease marker is a representation of a gene product that is present in all cells affected by disease either at an increased or decreased level relative to a normal cell
15 (*e.g.*, a cell of the same or similar type that is not substantially affected by disease). For example, a polynucleotide sequence in a library can be a polynucleotide that represents an mRNA, polypeptide, or other gene product encoded by the polynucleotide, that is either overexpressed or underexpressed in a cancerous breast cell affected by cancer relative to a normal (*i.e.*, substantially disease-free) breast cell.

20 The nucleotide sequence information of the library can be embodied in any suitable form, *e.g.*, electronic or biochemical forms. For example, a library of sequence information embodied in electronic form comprises an accessible computer data file (or, in biochemical form, a collection of nucleic acid molecules) that contains the representative nucleotide sequences of genes that are differentially expressed (*e.g.*, overexpressed or underexpressed)
25 as between, for example, i) a cancerous cell and a normal cell; ii) a cancerous cell and a dysplastic cell; iii) a cancerous cell and a cell affected by a disease or condition other than cancer; iv) a metastatic cancerous cell and a normal cell and/or non-metastatic cancerous cell; v) a malignant cancerous cell and a non-malignant cancerous cell (or a normal cell) and/or vi) a dysplastic cell relative to a normal cell. Other combinations and comparisons of
30 cells affected by various diseases or stages of disease will be readily apparent to the ordinarily skilled artisan. Biochemical embodiments of the library include a collection of nucleic acids that have the sequences of the genes in the library, where the nucleic acids can correspond to the entire gene in the library or to a fragment thereof, as described in greater detail below.

The polynucleotide libraries of the subject invention generally comprise sequence information of a plurality of polynucleotide sequences, where at least one of the polynucleotides has a sequence of any of sequence described herein. By plurality is meant at least 2, usually at least 3 and can include up to all of the sequences described herein. The length and number of polynucleotides in the library will vary with the nature of the library, *e.g.*, if the library is an oligonucleotide array, a cDNA array, a computer database of the sequence information, etc.

Where the library is an electronic library, the nucleic acid sequence information can be present in a variety of media. "Media" refers to a manufacture, other than an isolated nucleic acid molecule, that contains the sequence information of the present invention. Such a manufacture provides the genome sequence or a subset thereof in a form that can be examined by means not directly applicable to the sequence as it exists in a nucleic acid. For example, the nucleotide sequence of the present invention, *e.g.* the nucleic acid sequences of any of the polynucleotides of the sequences described herein, can be recorded on computer readable media, *e.g.* any medium that can be read and accessed directly by a computer. Such media include, but are not limited to: magnetic storage media, such as a floppy disc, a hard disc storage medium, and a magnetic tape; optical storage media such as CD-ROM; electrical storage media such as RAM and ROM; and hybrids of these categories such as magnetic/optical storage media.

One of skill in the art can readily appreciate how any of the presently known computer readable mediums can be used to create a manufacture comprising a recording of the present sequence information. "Recorded" refers to a process for storing information on computer readable medium, using any such methods as known in the art. Any convenient data storage structure can be chosen, based on the means used to access the stored information. A variety of data processor programs and formats can be used for storage, *e.g.* word processing text file, database format, *etc.* In addition to the sequence information, electronic versions of libraries comprising one or more sequence described herein can be provided in conjunction or connection with other computer-readable information and/or other types of computer-readable files (*e.g.*, searchable files, executable files, *etc.*, including, but not limited to, for example, search program software, *etc.*).

By providing the nucleotide sequence in computer readable form, the information can be accessed for a variety of purposes. Computer software to access sequence information (*e.g.* the NCBI sequence database) is publicly available. For example, the gapped BLAST (Altschul *et al.*, *Nucleic Acids Res.* (1997) 25:3389-3402) and BLAZE

(Brutlag *et al.*, *Comp. Chem.* (1993) 17:203) search algorithms on a Sybase system, or the TeraBLAST (TimeLogic, Crystal Bay, Nevada) program optionally running on a specialized computer platform available from TimeLogic, can be used to identify open reading frames (ORFs) within the genome that contain homology to ORFs from other organisms.

5 As used herein, "a computer-based system" refers to the hardware means, software means, and data storage means used to analyze the nucleotide sequence information of the present invention. The minimum hardware of the computer-based systems of the present invention comprises a central processing unit (CPU), input means, output means, and data storage means. A skilled artisan can readily appreciate that any one of the currently
10 available computer-based system are suitable for use in the present invention. The data storage means can comprise any manufacture comprising a recording of the present sequence information as described above, or a memory access means that can access such a manufacture.

 "Search means" refers to one or more programs implemented on the computer-based
15 system, to compare a target sequence or target structural motif, or expression levels of a polynucleotide in a sample, with the stored sequence information. Search means can be used to identify fragments or regions of the genome that match a particular target sequence or target motif. A variety of known algorithms are publicly known and commercially available, *e.g.* MacPattern (EMBL), TeraBLAST (TimeLogic), BLASTN and BLASTX (NCBI). A
20 "target sequence" can be any polynucleotide or amino acid sequence of six or more contiguous nucleotides or two or more amino acids, preferably from about 10 to 100 amino acids or from about 30 to 300 nt. A variety of means for comparing nucleic acids or polypeptides may be used to compare accomplish a sequence comparison (*e.g.*, to analyze target sequences, target motifs, or relative expression levels) with the data storage means. A
25 skilled artisan can readily recognize that any one of the publicly available homology search programs can be used to search the computer based systems of the present invention to compare of target sequences and motifs. Computer programs to analyze expression levels in a sample and in controls are also known in the art.

 A "target structural motif," or "target motif," refers to any rationally selected
30 sequence or combination of sequences in which the sequence(s) are chosen based on a three-dimensional configuration that is formed upon the folding of the target motif, or on consensus sequences of regulatory or active sites. There are a variety of target motifs known in the art. Protein target motifs include, but are not limited to, enzyme active sites and signal sequences, kinase domains, receptor binding domains, SH2 domains, SH3 domains,

phosphorylation sites, protein interaction domains, transmembrane domains, etc. Nucleic acid target motifs include, but are not limited to, hairpin structures, promoter sequences and other expression elements such as binding sites for transcription factors.

A variety of structural formats for the input and output means can be used to input
5 and output the information in the computer-based systems of the present invention. One
format for an output means ranks the relative expression levels of different polynucleotides.
Such presentation provides a skilled artisan with a ranking of relative expression levels to
determine a gene expression profile. A gene expression profile can be generated from, for
example, a cDNA library prepared from mRNA isolated from a test cell suspected of being
10 cancerous or pre-cancerous, comparing the sequences or partial sequences of the clones
against the sequences in an electronic database, where the sequences of the electronic
database represent genes differentially expressed in a cancerous cell, *e.g.*, a cancerous breast
cell. The number of clones having a sequence that has substantial similarity to a sequence
that represents a gene differentially expressed in a cancerous cell is then determined, and the
15 number of clones corresponding to each of such genes is determined. An increased number
of clones that correspond to differentially expressed gene is present in the cDNA library of
the test cell (relative to, for example, the number of clones expected in a cDNA of a normal
cell) indicates that the test cell is cancerous.

As discussed above, the "library" as used herein also encompasses biochemical
20 libraries of the polynucleotides of the sequences described herein, *e.g.*, collections of nucleic
acids representing the provided polynucleotides. The biochemical libraries can take a
variety of forms, *e.g.*, a solution of cDNAs, a pattern of probe nucleic acids stably
associated with a surface of a solid support (*i.e.*, an array) and the like. Of particular interest
are nucleic acid arrays in which one or more of the genes described herein is represented by
25 a sequence on the array. By array is meant an article of manufacture that has at least a
substrate with at least two distinct nucleic acid targets on one of its surfaces, where the
number of distinct nucleic acids can be considerably higher, typically being at least 10 nt,
usually at least 20 nt and often at least 25 nt. A variety of different array formats have been
developed and are known to those of skill in the art. The arrays of the subject invention find
30 use in a variety of applications, including gene expression analysis, drug screening, mutation
analysis and the like, as disclosed in the above-listed exemplary patent documents.

In addition to the above nucleic acid libraries, analogous libraries of polypeptides are
also provided, where the polypeptides of the library will represent at least a portion of the
polypeptides encoded by a gene corresponding to a sequence described herein.

DIAGNOSTIC AND OTHER METHODS INVOLVING DETECTION OF DIFFERENTIALLY EXPRESSED GENES

The present invention provides methods of using the polynucleotides described herein in, for example, diagnosis of cancer and classification of cancer cells according to expression profiles. In specific non-limiting embodiments, the methods are useful for detecting breast cancer cells, facilitating diagnosis of cancer and the severity of a cancer (e.g., tumor grade, tumor burden, and the like) in a subject, facilitating a determination of the prognosis of a subject, and assessing the responsiveness of the subject to therapy (e.g., by providing a measure of therapeutic effect through, for example, assessing tumor burden during or following a chemotherapeutic regimen). Detection can be based on detection of a polynucleotide that is differentially expressed in a breast cancer cell, and/or detection of a polypeptide encoded by a polynucleotide that is differentially expressed in a breast cancer cell ("a polypeptide associated with breast cancer"). The detection methods of the invention can be conducted *in vitro* or *in vivo*, on isolated cells, or in whole tissues or a bodily fluid, e.g., blood, plasma, serum, urine, and the like).

In general, methods of the invention involving detection of a gene product (e.g., mRNA, cDNA generated from such mRNA, and polypeptides) involve contacting a sample with a probe specific for the gene product of interest. "Probe" as used herein in such methods is meant to refer to a molecule that specifically binds a gene product of interest (e.g., the probe binds to the target gene product with a specificity sufficient to distinguish binding to target over non-specific binding to non-target (background) molecules). "Probes" include, but are not necessarily limited to, nucleic acid probes (e.g., DNA, RNA, modified nucleic acid, and the like), antibodies (e.g., antibodies, antibody fragments that retain binding to a target epitope, single chain antibodies, and the like), or other polypeptide, peptide, or molecule (e.g., receptor ligand) that specifically binds a target gene product of interest.

The probe and sample suspected of having the gene product of interest are contacted under conditions suitable for binding of the probe to the gene product. For example, contacting is generally for a time sufficient to allow binding of the probe to the gene product (e.g., from several minutes to a few hours), and at a temperature and conditions of osmolarity and the like that provide for binding of the probe to the gene product at a level that is sufficiently distinguishable from background binding of the probe (e.g., under conditions that minimize non-specific binding). Suitable conditions for probe-target gene

product binding can be readily determined using controls and other techniques available and known to one of ordinary skill in the art.

In this embodiment, the probe can be an antibody or other polypeptide, peptide, or molecule (*e.g.*, receptor ligand) that specifically binds a target polypeptide of interest.

5 The detection methods can be provided as part of a kit. Thus, the invention further provides kits for detecting the presence and/or a level of a polynucleotide that is differentially expressed in a breast cancer cell (*e.g.*, by detection of an mRNA encoded by the differentially expressed gene of interest), and/or a polypeptide encoded thereby, in a biological sample. Procedures using these kits can be performed by clinical laboratories, experimental laboratories, medical practitioners, or private individuals. The kits of the invention for detecting a polypeptide encoded by a polynucleotide that is differentially expressed in a breast cancer cell comprise a moiety that specifically binds the polypeptide, which may be a specific antibody. The kits of the invention for detecting a polynucleotide that is differentially expressed in a breast cancer cell comprise a moiety that specifically hybridizes to such a polynucleotide. The kit may optionally provide additional components that are useful in the procedure, including, but not limited to, buffers, developing reagents, labels, reacting surfaces, means for detection, control samples, standards, instructions, and interpretive information.

20 Detecting a polypeptide encoded by a polynucleotide that is differentially expressed in a breast cancer cell

In some embodiments, methods are provided for detecting breast cancer cell by detecting in a cell, particularly a breast cell, a polypeptide encoded by a gene differentially expressed in a breast cancer cell. Any of a variety of known methods can be used for detection, including, but not limited to, immunoassay, using an antibody specific for the encoded polypeptide, *e.g.*, by enzyme-linked immunosorbent assay (ELISA), radioimmunoassay (RIA), and the like; and functional assays for the encoded polypeptide, *e.g.*, binding activity or enzymatic activity.

For example, an immunofluorescence assay can be easily performed on cells without first isolating the encoded polypeptide. The cells are first fixed onto a solid support, such as a microscope slide or microtiter well. This fixing step can permeabilize the cell membrane. The permeabilization of the cell membrane permits the polypeptide-specific probe (*e.g.*, antibody) to bind. Alternatively, where the polypeptide is secreted or membrane-bound, or is otherwise accessible at the cell-surface (*e.g.*, receptors, and other molecule stably-

associated with the outer cell membrane or otherwise stably associated with the cell membrane, such permeabilization may not be necessary.

Next, the fixed cells are exposed to an antibody specific for the encoded polypeptide. To increase the sensitivity of the assay, the fixed cells may be further exposed to a second antibody, which is labeled and binds to the first antibody, which is specific for the encoded polypeptide. Typically, the secondary antibody is detectably labeled, e.g., with a fluorescent marker. The cells which express the encoded polypeptide will be fluorescently labeled and easily visualized under the microscope. See, for example, Hashido *et al.* (1992) *Biochem. Biophys. Res. Comm.* 187:1241-1248.

As will be readily apparent to the ordinarily skilled artisan upon reading the present specification, the detection methods and other methods described herein can be varied. Such variations are within the intended scope of the invention. For example, in the above detection scheme, the probe for use in detection can be immobilized on a solid support, and the test sample contacted with the immobilized probe. Binding of the test sample to the probe can then be detected in a variety of ways, e.g., by detecting a detectable label bound to the test sample.

The present invention further provides methods for detecting the presence of and/or measuring a level of a polypeptide in a biological sample, which polypeptide is encoded by a polynucleotide that represents a gene differentially expressed in cancer, particularly in a polynucleotide that represents a gene differentially cancer cell, using a probe specific for the encoded polypeptide. In this embodiment, the probe can be a an antibody or other polypeptide, peptide, or molecule (e.g., receptor ligand) that specifically binds a target polypeptide of interest.

The methods generally comprise: a) contacting the sample with an antibody specific for a differentially expressed polypeptide in a test cell; and b) detecting binding between the antibody and molecules of the sample. The level of antibody binding (either qualitative or quantitative) indicates the cancerous state of the cell. For example, where the differentially expressed gene is increased in cancerous cells, detection of an increased level of antibody binding to the test sample relative to antibody binding level associated with a normal cell indicates that the test cell is cancerous.

Suitable controls include a sample known not to contain the encoded polypeptide; and a sample contacted with an antibody not specific for the encoded polypeptide, e.g., an anti-idiotypic antibody. A variety of methods to detect specific antibody-antigen interactions are known in the art and can be used in the method, including, but not limited to, standard

immunohistological methods, immunoprecipitation, an enzyme immunoassay, and a radioimmunoassay.

In general, the specific antibody will be detectably labeled, either directly or indirectly. Direct labels include radioisotopes; enzymes whose products are detectable (e.g.,
5 luciferase, β -galactosidase, and the like); fluorescent labels (e.g., fluorescein isothiocyanate, rhodamine, phycoerythrin, and the like); fluorescence emitting metals, e.g., ^{152}Eu , or others of the lanthanide series, attached to the antibody through metal chelating groups such as EDTA; chemiluminescent compounds, e.g., luminol, isoluminol, acridinium salts, and the like; bioluminescent compounds, e.g., luciferin, aequorin (green fluorescent protein), and the
10 like.

The antibody may be attached (coupled) to an insoluble support, such as a polystyrene plate or a bead. Indirect labels include second antibodies specific for antibodies specific for the encoded polypeptide ("first specific antibody"), wherein the second antibody is labeled as described above; and members of specific binding pairs, e.g., biotin-avidin, and
15 the like. The biological sample may be brought into contact with and immobilized on a solid support or carrier, such as nitrocellulose, that is capable of immobilizing cells, cell particles, or soluble proteins. The support may then be washed with suitable buffers, followed by contacting with a detectably-labeled first specific antibody. Detection methods are known in the art and will be chosen as appropriate to the signal emitted by the detectable label.
20 Detection is generally accomplished in comparison to suitable controls, and to appropriate standards.

In some embodiments, the methods are adapted for use *in vivo*, e.g., to locate or identify sites where breast cancer cells are present. In these embodiments, a detectably-labeled moiety, e.g., an antibody, which is specific for a breast cancer-associated polypeptide
25 is administered to an individual (e.g., by injection), and labeled cells are located using standard imaging techniques, including, but not limited to, magnetic resonance imaging, computed tomography scanning, and the like. In this manner, breast cancer cells are differentially labeled.

Detecting a polynucleotide that represents a gene differentially expressed in a breast 30 cancer cell

In some embodiments, methods are provided for detecting a breast cancer cell by detecting expression in the cell of a transcript or that is differentially expressed in a breast cancer cell. Any of a variety of known methods can be used for detection, including, but not limited to, detection of a transcript by hybridization with a polynucleotide that hybridizes to

a polynucleotide that is differentially expressed in a breast cancer cell; detection of a transcript by a polymerase chain reaction using specific oligonucleotide primers; *in situ* hybridization of a cell using as a probe a polynucleotide that hybridizes to a gene that is differentially expressed in a breast cancer cell and the like.

5 In many embodiments, the levels of a subject gene product are measured. By measured is meant qualitatively or quantitatively estimating the level of the gene product in a first biological sample either directly (e.g. by determining or estimating absolute levels of gene product) or relatively by comparing the levels to a second control biological sample. In many embodiments the second control biological sample is obtained from an individual not
10 having not having breast cancer. As will be appreciated in the art, once a standard control level of gene expression is known, it can be used repeatedly as a standard for comparison. Other control samples include samples of cancerous breast tissue.

 The methods can be used to detect and/or measure mRNA levels of a gene that is differentially expressed in a breast cancer cell. In some embodiments, the methods
15 comprise: a) contacting a sample with a polynucleotide that corresponds to a differentially expressed gene described herein under conditions that allow hybridization; and b) detecting hybridization, if any. Detection of differential hybridization, when compared to a suitable control, is an indication of the presence in the sample of a polynucleotide that is differentially expressed in a breast cancer cell. Appropriate controls include, for example, a
20 sample that is known not to contain a polynucleotide that is differentially expressed in a breast cancer cell. Conditions that allow hybridization are known in the art, and have been described in more detail above.

 Detection can also be accomplished by any known method, including, but not limited to, *in situ* hybridization, PCR (polymerase chain reaction), RT-PCR (reverse transcription-
25 PCR), and "Northern" or RNA blotting, arrays, microarrays, etc, or combinations of such techniques, using a suitably labeled polynucleotide. A variety of labels and labeling methods for polynucleotides are known in the art and can be used in the assay methods of the invention. Specific hybridization can be determined by comparison to appropriate controls.

30 Polynucleotide generally comprising at least 12 contiguous nt of a polynucleotide provided herein, as shown in the Sequence Listing or of the sequences of the genes corresponding to the polynucleotides of the Sequence Listing, are used for a variety of purposes, such as probes for detection of and/or measurement of, transcription levels of a polynucleotide that is differentially expressed in a breast cancer cell. Additional disclosure

about preferred regions of the disclosed polynucleotide sequences is found in the Examples. A probe that hybridizes specifically to a polynucleotide disclosed herein should provide a detection signal at least 2-, 5-, 10-, or 20-fold higher than the background hybridization provided with other unrelated sequences. It should be noted that "probe" as used in this context of detection of nucleic acid is meant to refer to a polynucleotide sequence used to detect a differentially expressed gene product in a test sample. As will be readily appreciated by the ordinarily skilled artisan, the probe can be detectably labeled and contacted with, for example, an array comprising immobilized polynucleotides obtained from a test sample (*e.g.*, mRNA). Alternatively, the probe can be immobilized on an array and the test sample detectably labeled. These and other variations of the methods of the invention are well within the skill in the art and are within the scope of the invention.

Labeled nucleic acid probes may be used to detect expression of a gene corresponding to the provided polynucleotide. In Northern blots, mRNA is separated electrophoretically and contacted with a probe. A probe is detected as hybridizing to an mRNA species of a particular size. The amount of hybridization can be quantitated to determine relative amounts of expression, for example under a particular condition. Probes are used for in situ hybridization to cells to detect expression. Probes can also be used *in vivo* for diagnostic detection of hybridizing sequences. Probes are typically labeled with a radioactive isotope. Other types of detectable labels can be used such as chromophores, fluorophores, and enzymes. Other examples of nucleotide hybridization assays are described in WO92/02526 and USPN 5,124,246.

PCR is another means for detecting small amounts of target nucleic acids, methods for which may be found in Sambrook, *et al.* Molecular Cloning: A Laboratory Manual, CSH Press 1989, pp.14.2-14.33.

A detectable label may be included in the amplification reaction. Suitable detectable labels include fluorochromes, (*e.g.* fluorescein isothiocyanate (FITC), rhodamine, Texas Red, phycoerythrin, allophycocyanin, 6-carboxyfluorescein (6-FAM), 2',7'-dimethoxy-4',5'-dichloro-6-carboxyfluorescein, 6-carboxy-X-rhodamine (ROX), 6-carboxy-2',4',7',4,7-hexachlorofluorescein (HEX), 5-carboxyfluorescein (5-FAM) or N,N,N',N'-tetramethyl-6-carboxyrhodamine (TAMRA)), radioactive labels, (*e.g.* ^{32}P , ^{35}S , ^3H , *etc.*), and the like. The label may be a two stage system, where the polynucleotides is conjugated to biotin, haptens, *etc.* having a high affinity binding partner, *e.g.* avidin, specific antibodies, *etc.*, where the binding partner is conjugated to a detectable label. The label may be conjugated to one or

both of the primers. Alternatively, the pool of nucleotides used in the amplification is labeled, so as to incorporate the label into the amplification product.

Arrays

Polynucleotide arrays provide a high throughput technique that can assay a large
5 number of polynucleotides or polypeptides in a sample. This technology can be used as a tool to test for differential expression.

A variety of methods of producing arrays, as well as variations of these methods, are known in the art and contemplated for use in the invention. For example, arrays can be created by spotting polynucleotide probes onto a substrate (*e.g.*, glass, nitrocellulose, *etc.*) in
10 a two-dimensional matrix or array having bound probes. The probes can be bound to the substrate by either covalent bonds or by non-specific interactions, such as hydrophobic interactions.

Samples of polynucleotides can be detectably labeled (*e.g.*, using radioactive or fluorescent labels) and then hybridized to the probes. Double stranded polynucleotides,
15 comprising the labeled sample polynucleotides bound to probe polynucleotides, can be detected once the unbound portion of the sample is washed away. Alternatively, the polynucleotides of the test sample can be immobilized on the array, and the probes detectably labeled. Techniques for constructing arrays and methods of using these arrays are described in, for example, Schena *et al.* (1996) *Proc Natl Acad Sci U S A.* 93(20):10614-9;
20 Schena *et al.* (1995) *Science* 270(5235):467-70; Shalon *et al.* (1996) *Genome Res.* 6(7):639-45, USPN 5,807,522, EP 799 897; WO 97/29212; WO 97/27317; EP 785 280; WO 97/02357; USPN 5,593,839; USPN 5,578,832; EP 728 520; USPN 5,599,695; EP 721 016; USPN 5,556,752; WO 95/22058; and USPN 5,631,734. In most embodiments, the "probe" is detectably labeled. In other embodiments, the probe is immobilized on the array and not
25 detectably labeled.

Arrays can be used, for example, to examine differential expression of genes and can be used to determine gene function. For example, arrays can be used to detect differential expression of a gene corresponding to a polynucleotide described herein, where expression is compared between a test cell and control cell (*e.g.*, cancer cells and normal cells). For
30 example, high expression of a particular message in a cancer cell, which is not observed in a corresponding normal cell, can indicate a cancer specific gene product. Exemplary uses of arrays are further described in, for example, Pappalarado *et al.*, *Sem. Radiation Oncol.* (1998) 8:217; and Ramsay, *Nature Biotechnol.* (1998) 16:40. Furthermore, many variations on methods of detection using arrays are well within the skill in the art and within the scope

of the present invention. For example, rather than immobilizing the probe to a solid support, the test sample can be immobilized on a solid support which is then contacted with the probe.

5 DIAGNOSIS, PROGNOSIS, ASSESSMENT OF THERAPY (THERAMETRICS), AND
MANAGEMENT OF CANCER

 The polynucleotides described herein, as well as their gene products and
corresponding genes and gene products, are of particular interest as genetic or biochemical
markers (e.g., in blood or tissues) that will detect the earliest changes along the
10 carcinogenesis pathway and/or to monitor the efficacy of various therapies and preventive
interventions.

 For example, the level of expression of certain polynucleotides can be indicative of a
poorer prognosis, and therefore warrant more aggressive chemo- or radio-therapy for a
patient or vice versa. The correlation of novel surrogate tumor specific features with
15 response to treatment and outcome in patients can define prognostic indicators that allow the
design of tailored therapy based on the molecular profile of the tumor. These therapies
include antibody targeting, antagonists (e.g., small molecules), and gene therapy.

 Determining expression of certain polynucleotides and comparison of a patient's
profile with known expression in normal tissue and variants of the disease allows a
20 determination of the best possible treatment for a patient, both in terms of specificity of
treatment and in terms of comfort level of the patient. Surrogate tumor markers, such as
polynucleotide expression, can also be used to better classify, and thus diagnose and treat,
different forms and disease states of cancer. Two classifications widely used in oncology
that can benefit from identification of the expression levels of the genes corresponding to the
25 polynucleotides described herein are staging of the cancerous disorder, and grading the
nature of the cancerous tissue.

 The polynucleotides that correspond to differentially expressed genes, as well as their
encoded gene products, can be useful to monitor patients having or susceptible to cancer to
detect potentially malignant events at a molecular level before they are detectable at a gross
30 morphological level. In addition, the polynucleotides described herein, as well as the genes
corresponding to such polynucleotides, can be useful as therametrics, e.g., to assess the
effectiveness of therapy by using the polynucleotides or their encoded gene products, to
assess, for example, tumor burden in the patient before, during, and after therapy.

Furthermore, a polynucleotide identified as corresponding to a gene that is differentially expressed in, and thus is important for, one type of cancer can also have implications for development or risk of development of other types of cancer, e.g., where a polynucleotide represents a gene differentially expressed across various cancer types. Thus, for example, expression of a polynucleotide corresponding to a gene that has clinical implications for breast cancer can also have clinical implications for metastatic breast cancer, colon cancer, or ovarian cancer.

Staging. Staging is a process used by physicians to describe how advanced the cancerous state is in a patient. Staging assists the physician in determining a prognosis, planning treatment and evaluating the results of such treatment. Staging systems vary with the types of cancer, but generally involve the following "TNM" system: the type of tumor, indicated by T; whether the cancer has metastasized to nearby lymph nodes, indicated by N; and whether the cancer has metastasized to more distant parts of the body, indicated by M. Generally, if a cancer is only detectable in the area of the primary lesion without having spread to any lymph nodes it is called Stage I. If it has spread only to the closest lymph nodes, it is called Stage II. In Stage III, the cancer has generally spread to the lymph nodes in near proximity to the site of the primary lesion. Cancers that have spread to a distant part of the body, such as the liver, bone, brain or other site, are Stage IV, the most advanced stage.

The polynucleotides and corresponding genes and gene products described herein can facilitate fine-tuning of the staging process by identifying markers for the aggressiveness of a cancer, e.g. the metastatic potential, as well as the presence in different areas of the body. Thus, a Stage II cancer with a polynucleotide signifying a high metastatic potential cancer can be used to change a borderline Stage II tumor to a Stage III tumor, justifying more aggressive therapy. Conversely, the presence of a polynucleotide signifying a lower metastatic potential allows more conservative staging of a tumor.

One type of breast cancer is ductal carcinoma in situ (DCIS): DCIS is when the breast cancer cells are completely contained within the breast ducts (the channels in the breast that carry milk to the nipple), and have not spread into the surrounding breast tissue. This may also be referred to as non-invasive or intraductal cancer, as the cancer cells have not yet spread into the surrounding breast tissue and so usually have not spread into any other part of the body.

Lobular carcinoma in situ breast cancer (LCIS) means that cell changes are found in the lining of the lobules of the breast. It can be present in both breasts. It is also referred to as non-invasive cancer as it has not spread into the surrounding breast tissue.

Invasive breast cancer can be staged as follows: Stage 1 tumours: these measure less than two centimetres. The lymph glands in the armpit are not affected and there are no signs that the cancer has spread elsewhere in the body; Stage 2 tumours: these measure between two and five centimetres, or the lymph glands in the armpit are affected, or both. However, there are no signs that the cancer has spread further; Stage 3 tumours: these are larger than five centimetres and may be attached to surrounding structures such as the muscle or skin. The lymph glands are usually affected, but there are no signs that the cancer has spread beyond the breast or the lymph glands in the armpit; Stage 4 tumours: these are of any size, but the lymph glands are usually affected and the cancer has spread to other parts of the body. This is secondary breast cancer.

Grading of cancers. Grade is a term used to describe how closely a tumor resembles normal tissue of its same type. The microscopic appearance of a tumor is used to identify tumor grade based on parameters such as cell morphology, cellular organization, and other markers of differentiation. As a general rule, the grade of a tumor corresponds to its rate of growth or aggressiveness, with undifferentiated or high-grade tumors generally being more aggressive than well-differentiated or low-grade tumors.

The polynucleotides of the Sequence Listing, and their corresponding genes and gene products, can be especially valuable in determining the grade of the tumor, as they not only can aid in determining the differentiation status of the cells of a tumor, they can also identify factors other than differentiation that are valuable in determining the aggressiveness of a tumor, such as metastatic potential.

Low grade means that the cancer cells look very like the normal cells of the breast. They are usually slowly growing and are less likely to spread. In high grade tumors the cells look very abnormal. They are likely to grow more quickly and are more likely to spread.

Assessment of proliferation of cells in tumor. The differential expression level of the polynucleotides described herein can facilitate assessment of the rate of proliferation of tumor cells, and thus provide an indicator of the aggressiveness of the rate of tumor growth. For example, assessment of the relative expression levels of genes involved in cell cycle can provide an indication of cellular proliferation, and thus serve as a marker of proliferation.

Detection of breast cancer.

The polynucleotides corresponding to genes that exhibit the appropriate expression pattern can be used to detect breast cancer in a subject. Breast cancer is one of the most common neoplasms in women, and prevention and early detection are key factors in controlling and curing breast cancer. The expression of appropriate polynucleotides can be used in the diagnosis, prognosis and management of breast cancer. Detection of breast cancer can be determined using expression levels of any of these sequences alone or in combination with the levels of expression of other known cancer genes. Determination of the aggressive nature and/or the metastatic potential of a breast cancer can be determined by comparing levels of one or more gene products of the genes corresponding to the polynucleotides described herein, and comparing total levels of another sequence known to vary in cancerous tissue, *e.g.*, expression of p53, DCC, ras, FAP (see, *e.g.*, Fearon ER, *et al.*, *Cell* (1990) 61(5):759; Hamilton SR *et al.*, *Cancer* (1993) 72:957; Bodmer W, *et al.*, *Nat Genet.* (1994) 4(3):217; Fearon ER, *Ann N Y Acad Sci.* (1995) 768:101). For example, development of breast cancer can be detected by examining the level of expression of a gene corresponding to a polynucleotides described herein to the levels of oncogenes (*e.g.* ras) or tumor suppressor genes (*e.g.* FAP or p53). Thus expression of specific marker polynucleotides can be used to discriminate between normal and cancerous breast tissue, to discriminate between breast cancers with different cells of origin, to discriminate between breast cancers with different potential metastatic rates, etc. For a review of other markers of cancer, see, *e.g.*, Hanahan et al. (2000) *Cell* 100:57-70.

Treatment of breast cancer

The invention further provides methods for reducing growth of breast cancer cells. The methods provide for decreasing the expression of a gene that is differentially expressed in a breast cancer cell or decreasing the level of and/or decreasing an activity of a breast cancer-associated polypeptide. In general, the methods comprise contacting a breast cancer cell with a substance that modulates (1) expression of a gene that is differentially expressed in breast cancer; or (2) a level of and/or an activity of a breast cancer-associated polypeptide.

“Reducing growth of breast cancer cells” includes, but is not limited to, reducing proliferation of breast cancer cells, and reducing the incidence of a non-cancerous breast cell becoming a cancerous breast cell. Whether a reduction in breast cancer cell growth has been achieved can be readily determined using any known assay, including, but not limited to, [³H]-thymidine incorporation; counting cell number over a period of time; detecting and/or measuring a marker associated with breast cancer (*e.g.*, PSA).

The present invention provides methods for treating breast cancer, generally comprising administering to an individual in need thereof a substance that reduces breast cancer cell growth, in an amount sufficient to reduce breast cancer cell growth and treat the breast cancer. Whether a substance, or a specific amount of the substance, is effective in
5 treating breast cancer can be assessed using any of a variety of known diagnostic assays for breast cancer, including, but not limited to, proctoscopy, rectal examination, biopsy, contrast radiographic studies, CAT scan, and detection of a tumor marker associated with breast cancer in the blood of the individual (*e.g.*, PSA (breast-specific antigen)). The substance can be administered systemically or locally. Thus, in some embodiments, the substance is
10 administered locally, and breast cancer growth is decreased at the site of administration. Local administration may be useful in treating, *e.g.*, a solid tumor.

A substance that reduces breast cancer cell growth can be targeted to a breast cancer cell. Thus, in some embodiments, the invention provides a method of delivering a drug to a breast cancer cell, comprising administering a drug-antibody complex to a subject, wherein
15 the antibody is specific for a breast cancer-associated polypeptide, and the drug is one that reduces breast cancer cell growth, a variety of which are known in the art. Targeting can be accomplished by coupling (*e.g.*, linking, directly or via a linker molecule, either covalently or non-covalently, so as to form a drug-antibody complex) a drug to an antibody specific for a breast cancer-associated polypeptide. Methods of coupling a drug to an antibody are well
20 known in the art and need not be elaborated upon herein.

Tumor classification and patient stratification

The invention further provides for methods of classifying tumors, and thus grouping or "stratifying" patients, according to the expression profile of selected differentially expressed genes in a tumor. Differentially expressed genes can be analyzed for correlation
25 with other differentially expressed genes in a single tumor type or across tumor types. Genes that demonstrate consistent correlation in expression profile in a given cancer cell type (*e.g.*, in a breast cancer cell or type of breast cancer) can be grouped together, *e.g.*, when one gene is overexpressed in a tumor, a second gene is also usually overexpressed. Tumors can then be classified according to the expression profile of one or more genes
30 selected from one or more groups.

The tumor of each patient in a pool of potential patients can be classified as described above. Patients having similarly classified tumors can then be selected for participation in an investigative or clinical trial of a cancer therapeutic where a homogeneous population is desired. The tumor classification of a patient can also be used in assessing the efficacy of a

cancer therapeutic in a heterogeneous patient population. In addition, therapy for a patient having a tumor of a given expression profile can then be selected accordingly.

In another embodiment, differentially expressed gene products (*e.g.*, polypeptides or polynucleotides encoding such polypeptides) may be effectively used in treatment through vaccination. The growth of cancer cells is naturally limited in part due to immune surveillance. Stimulation of the immune system using a particular tumor-specific antigen enhances the effect towards the tumor expressing the antigen. An active vaccine comprising a polypeptide encoded by the cDNA of this invention would be appropriately administered to subjects having an alteration, *e.g.*, overabundance, of the corresponding RNA, or those predisposed for developing cancer cells with an alteration of the same RNA. Polypeptide antigens are typically combined with an adjuvant as part of a vaccine composition. The vaccine is preferably administered first as a priming dose, and then again as a boosting dose, usually at least four weeks later. Further boosting doses may be given to enhance the effect. The dose and its timing are usually determined by the person responsible for the treatment.

The invention also encompasses the selection of a therapeutic regimen based upon the expression profile of differentially expressed genes in the patient's tumor. For example, a tumor can be analyzed for its expression profile of the genes corresponding to SEQ ID NOS:1-499 as described herein, *e.g.*, the tumor is analyzed to determine which genes are expressed at elevated levels or at decreased levels relative to normal cells of the same tissue type. The expression patterns of the tumor are then compared to the expression patterns of tumors that respond to a selected therapy. Where the expression profiles of the test tumor cell and the expression profile of a tumor cell of known drug responsivity at least substantially match (*e.g.*, selected sets of genes at elevated levels in the tumor of known drug responsivity and are also at elevated levels in the test tumor cell), then the therapeutic agent selected for therapy is the drug to which tumors with that expression pattern respond.

Pattern matching in diagnosis using arrays

In another embodiment, the diagnostic and/or prognostic methods of the invention involve detection of expression of a selected set of genes in a test sample to produce a test expression pattern (TEP). The TEP is compared to a reference expression pattern (REP), which is generated by detection of expression of the selected set of genes in a reference sample (*e.g.*, a positive or negative control sample). The selected set of genes includes at least one of the genes of the invention, which genes correspond to the polynucleotide sequences described herein. Of particular interest is a selected set of genes that includes gene differentially expressed in the disease for which the test sample is to be screened.

IDENTIFICATION OF THERAPEUTIC TARGETS AND ANTI-CANCER THERAPEUTIC AGENTS

The present invention also encompasses methods for identification of agents having the ability to modulate activity of a differentially expressed gene product, as well as methods for identifying a differentially expressed gene product as a therapeutic target for treatment of cancer, especially breast cancer.

Identification of compounds that modulate activity of a differentially expressed gene product can be accomplished using any of a variety of drug screening techniques. Such agents are candidates for development of cancer therapies. Of particular interest are screening assays for agents that have tolerable toxicity for normal, non-cancerous human cells. The screening assays of the invention are generally based upon the ability of the agent to modulate an activity of a differentially expressed gene product and/or to inhibit or suppress phenomenon associated with cancer (*e.g.*, cell proliferation, colony formation, cell cycle arrest, metastasis, and the like).

Screening of candidate agents

Screening assays can be based upon any of a variety of techniques readily available and known to one of ordinary skill in the art. In general, the screening assays involve contacting a cancerous cell (preferably a cancerous cell such as a cancerous breast cell) with a candidate agent, and assessing the effect upon biological activity of a differentially expressed gene product. The effect upon a biological activity can be detected by, for example, detection of expression of a gene product of a differentially expressed gene (*e.g.*, a decrease in mRNA or polypeptide levels, would in turn cause a decrease in biological activity of the gene product). Alternatively or in addition, the effect of the candidate agent can be assessed by examining the effect of the candidate agent in a functional assay. For example, where the differentially expressed gene product is an enzyme, then the effect upon biological activity can be assessed by detecting a level of enzymatic activity associated with the differentially expressed gene product. The functional assay will be selected according to the differentially expressed gene product. In general, where the differentially expressed gene is increased in expression in a cancerous cell, agents of interest are those that decrease activity of the differentially expressed gene product.

Assays described *infra* can be readily adapted in the screening assay embodiments of the invention. Exemplary assays useful in screening candidate agents include, but are not limited to, hybridization-based assays (*e.g.*, use of nucleic acid probes or primers to assess expression levels), antibody-based assays (*e.g.*, to assess levels of polypeptide gene products), binding assays (*e.g.*, to detect interaction of a candidate agent with a differentially

expressed polypeptide, which assays may be competitive assays where a natural or synthetic ligand for the polypeptide is available), and the like. Additional exemplary assays include, but are not necessarily limited to, cell proliferation assays, antisense knockout assays, assays to detect inhibition of cell cycle, assays of induction of cell death/apoptosis, and the like.

- 5 Generally such assays are conducted *in vitro*, but many assays can be adapted for *in vivo* analyses, *e.g.*, in an animal model of the cancer.

Identification of therapeutic targets

- 10 In another embodiment, the invention contemplates identification of differentially expressed genes and gene products as therapeutic targets. In some respects, this is the converse of the assays described above for identification of agents having activity in modulating (*e.g.*, decreasing or increasing) activity of a differentially expressed gene product.

- 15 In this embodiment, therapeutic targets are identified by examining the effect(s) of an agent that can be demonstrated or has been demonstrated to modulate a cancerous phenotype (*e.g.*, inhibit or suppress or prevent development of a cancerous phenotype). Such agents are generally referred to herein as an "anti-cancer agent", which agents encompass chemotherapeutic agents. For example, the agent can be an antisense oligonucleotide that is specific for a selected gene transcript. For example, the antisense oligonucleotide may have a sequence corresponding to a sequence of a differentially expressed gene described herein, *e.g.*, a sequence of one of SEQ ID NOS:1-499.

- 20 Assays for identification of therapeutic targets can be conducted in a variety of ways using methods that are well known to one of ordinary skill in the art. For example, a test cancerous cell that expresses or overexpresses a differentially expressed gene is contacted with an anti-cancer agent, the effect upon a cancerous phenotype and a biological activity of the candidate gene product assessed. The biological activity of the candidate gene product can be assayed by examining, for example, modulation of expression of a gene encoding the candidate gene product (*e.g.*, as detected by, for example, an increase or decrease in transcript levels or polypeptide levels), or modulation of an enzymatic or other activity of the gene product. The cancerous phenotype can be, for example, cellular proliferation, loss of contact inhibition of growth (*e.g.*, colony formation), tumor growth (*in vitro* or *in vivo*), and the like. Alternatively or in addition, the effect of modulation of a biological activity of the candidate target gene upon cell death/apoptosis or cell cycle regulation can be assessed.

Inhibition or suppression of a cancerous phenotype, or an increase in cell death or apoptosis as a result of modulation of biological activity of a candidate gene product

indicates that the candidate gene product is a suitable target for cancer therapy. Assays described *infra* can be readily adapted for assays for identification of therapeutic targets. Generally such assays are conducted *in vitro*, but many assays can be adapted for *in vivo* analyses, *e.g.*, in an appropriate, art-accepted animal model of the cancer.

5 Candidate agents

The term "agent" as used herein describes any molecule, *e.g.* protein or pharmaceutical, with the capability of modulating a biological activity of a gene product of a differentially expressed gene. Generally a plurality of assay mixtures are run in parallel with different agent concentrations to obtain a differential response to the various concentrations.

10 Typically, one of these concentrations serves as a negative control, *i.e.* at zero concentration or below the level of detection.

Candidate agents encompass numerous chemical classes, though typically they are organic molecules, preferably small organic compounds having a molecular weight of more than 50 and less than about 2,500 daltons. Candidate agents comprise functional groups
15 necessary for structural interaction with proteins, particularly hydrogen bonding, and typically include at least an amine, carbonyl, hydroxyl or carboxyl group, preferably at least two of the functional chemical groups. The candidate agents often comprise cyclical carbon or heterocyclic structures and/or aromatic or polyaromatic structures substituted with one or more of the above functional groups. Candidate agents are also found among biomolecules
20 including, but not limited to: peptides, saccharides, fatty acids, steroids, purines, pyrimidines, derivatives, structural analogs or combinations thereof.

Candidate agents are obtained from a wide variety of sources including libraries of synthetic or natural compounds. For example, numerous means are available for random and directed synthesis of a wide variety of organic compounds and biomolecules, including
25 expression of randomized oligonucleotides and oligopeptides. Alternatively, libraries of natural compounds in the form of bacterial, fungal, plant and animal extracts (including extracts from human tissue to identify endogenous factors affecting differentially expressed gene products) are available or readily produced. Additionally, natural or synthetically produced libraries and compounds are readily modified through conventional chemical,
30 physical and biochemical means, and may be used to produce combinatorial libraries. Known pharmacological agents may be subjected to directed or random chemical modifications, such as acylation, alkylation, esterification, amidification, *etc.* to produce structural analogs.

Exemplary candidate agents of particular interest include, but are not limited to, antisense and RNAi polynucleotides, and antibodies, soluble receptors, and the like. Antibodies and soluble receptors are of particular interest as candidate agents where the target differentially expressed gene product is secreted or accessible at the cell-surface (e.g.,
5 receptors and other molecule stably-associated with the outer cell membrane).

For method that involve RNAi (RNA interference), a double stranded RNA (dsRNA) molecule is usually used. The dsRNA is prepared to be substantially identical to at least a segment of a subject polynucleotide (e.g. a cDNA or gene). In general, the dsRNA is selected to have at least 70%, 75%, 80%, 85% or 90% sequence identity with the subject
10 polynucleotide over at least a segment of the candidate gene. In other instances, the sequence identity is even higher, such as 95%, 97% or 99%, and in still other instances, there is 100% sequence identity with the subject polynucleotide over at least a segment of the subject polynucleotide. The size of the segment over which there is sequence identity can vary depending upon the size of the subject polynucleotide. In general, however, there is
15 substantial sequence identity over at least 15, 20, 25, 30, 35, 40 or 50 nucleotides. In other instances, there is substantial sequence identity over at least 100, 200, 300, 400, 500 or 1000 nucleotides; in still other instances, there is substantial sequence identity over the entire length of the subject polynucleotide, i.e., the coding and non-coding region of the candidate gene.

20 Because only substantial sequence similarity between the subject polynucleotide and the dsRNA is necessary, sequence variations between these two species arising from genetic mutations, evolutionary divergence and polymorphisms can be tolerated. Moreover, as described further infra, the dsRNA can include various modified or nucleotide analogs.

Usually the dsRNA consists of two separate complementary RNA strands. However,
25 in some instances, the dsRNA may be formed by a single strand of RNA that is self-complementary, such that the strand loops back upon itself to form a hairpin loop. Regardless of form, RNA duplex formation can occur inside or outside of a cell.

The size of the dsRNA that is utilized varies according to the size of the subject polynucleotide whose expression is to be suppressed and is sufficiently long to be effective
30 in reducing expression of the subject polynucleotide in a cell. Generally, the dsRNA is at least 10-15 nucleotides long. In certain applications, the dsRNA is less than 20, 21, 22, 23, 24 or 25 nucleotides in length. In other instances, the dsRNA is at least 50, 100, 150 or 200 nucleotides in length. The dsRNA can be longer still in certain other applications, such as at least 300, 400, 500 or 600 nucleotides. Typically, the dsRNA is not longer than 3000

nucleotides. The optimal size for any particular subject polynucleotide can be determined by one of ordinary skill in the art without undue experimentation by varying the size of the dsRNA in a systematic fashion and determining whether the size selected is effective in interfering with expression of the subject polynucleotide.

5 dsRNA can be prepared according to any of a number of methods that are known in the art, including *in vitro* and *in vivo* methods, as well as by synthetic chemistry approaches.

In vitro methods. Certain methods generally involve inserting the segment corresponding to the candidate gene that is to be transcribed between a promoter or pair of promoters that are oriented to drive transcription of the inserted segment and then utilizing
10 an appropriate RNA polymerase to carry out transcription. One such arrangement involves positioning a DNA fragment corresponding to the candidate gene or segment thereof into a vector such that it is flanked by two opposable polymerase-specific promoters that can be same or different. Transcription from such promoters produces two complementary RNA strands that can subsequently anneal to form the desired dsRNA. Exemplary plasmids for
15 use in such systems include the plasmid (PCR 4.0 TOPO) (available from Invitrogen). Another example is the vector pGEM-T (Promega, Madison, WI) in which the oppositely oriented promoters are T7 and SP6; the T3 promoter can also be utilized.

In a second arrangement, DNA fragments corresponding to the segment of the subject polynucleotide that is to be transcribed is inserted both in the sense and antisense
20 orientation downstream of a single promoter. In this system, the sense and antisense fragments are cotranscribed to generate a single RNA strand that is self-complementary and thus can form dsRNA.

Various other *in vitro* methods have been described. Examples of such methods include, but are not limited to, the methods described by Sadher et al. (Biochem. Int.
25 14:1015, 1987); by Bhattacharyya (Nature 343:484, 1990); and by Livache, et al. (U.S. Patent No. 5,795,715), each of which is incorporated herein by reference in its entirety.

Single-stranded RNA can also be produced using a combination of enzymatic and organic synthesis or by total organic synthesis. The use of synthetic chemical methods enable one to introduce desired modified nucleotides or nucleotide analogs into the dsRNA.

30 *In vivo methods.* dsRNA can also be prepared *in vivo* according to a number of established methods (see, e.g., Sambrook, et al. (1989) Molecular Cloning: A Laboratory Manual, 2nd ed.; Transcription and Translation (B.D. Hames, and S.J. Higgins, Eds., 1984); DNA Cloning, volumes I and II (D.N. Glover, Ed., 1985); and Oligonucleotide Synthesis (M.J. Gait, Ed., 1984, each of which is incorporated herein by reference in its entirety).

Once the single-stranded RNA has been formed, the complementary strands are allowed to anneal to form duplex RNA. Transcripts are typically treated with DNAase and further purified according to established protocols to remove proteins. Usually such purification methods are not conducted with phenol:chloroform. The resulting purified transcripts are subsequently dissolved in RNAase free water or a buffer of suitable composition.

dsRNA is generated by annealing the sense and anti-sense RNA in vitro. Generally, the strands are initially denatured to keep the strands separate and to avoid self-annealing. During the annealing process, typically certain ratios of the sense and antisense strands are combined to facilitate the annealing process. In some instances, a molar ratio of sense to antisense strands of 3:7 is used; in other instances, a ratio of 4:6 is utilized; and in still other instances, the ratio is 1:1.

The buffer composition utilized during the annealing process can in some instances affect the efficacy of the annealing process and subsequent transfection procedure. While some have indicated that the buffered solution used to carry out the annealing process should include a potassium salt such as potassium chloride (e.g. at a concentration of about 80 mM). In some embodiments, the buffer is substantially potassium free. Once single-stranded RNA has annealed to form duplex RNA, typically any single-strand overhangs are removed using an enzyme that specifically cleaves such overhangs (e.g., RNAase A or RNAase T).

Once the dsRNA has been formed, it is introduced into a reference cell, which can include an individual cell or a population of cells (e.g., a tissue, an embryo and an entire organism). The cell can be from essentially any source, including animal, plant, viral, bacterial, fungal and other sources. If a tissue, the tissue can include dividing or nondividing and differentiated or undifferentiated cells. Further, the tissue can include germ line cells and somatic cells. Examples of differentiated cells that can be utilized include, but are not limited to, neurons, glial cells, blood cells, megakaryocytes, lymphocytes, macrophages, neutrophils, eosinophils, basophils, mast cells, leukocytes, granulocytes, keratinocytes, adipocytes, osteoblasts, osteoclasts, hepatocytes, cells of the endocrine or exocrine glands, fibroblasts, myocytes, cardiomyocytes, and endothelial cells. The cell can be an individual cell of an embryo, and can be a blastocyte or an oocyte.

Certain methods are conducted using model systems for particular cellular states (e.g., a disease). For instance, certain methods provided herein are conducted with a cancer cell lines that serves as a model system for investigating genes that are correlated with various cancers.

A number of options can be utilized to deliver the dsRNA into a cell or population of cells such as in a cell culture, tissue or embryo. For instance, RNA can be directly introduced intracellularly. Various physical methods are generally utilized in such instances, such as administration by microinjection (see, e.g., Zernicka-Goetz, et al. (1997)

5 Development 124:1133-1137; and Wianny, et al. (1998) Chromosoma 107: 430-439).

Other options for cellular delivery include permeabilizing the cell membrane and electroporation in the presence of the dsRNA, liposome-mediated transfection, or transfection using chemicals such as calcium phosphate. A number of established gene therapy techniques can also be utilized to introduce the dsRNA into a cell. By introducing a
10 viral construct within a viral particle, for instance, one can achieve efficient introduction of an expression construct into the cell and transcription of the RNA encoded by the construct.

If the dsRNA is to be introduced into an organism or tissue, gene gun technology is an option that can be employed. This generally involves immobilizing the dsRNA on a gold particle which is subsequently fired into the desired tissue. Research has also shown that
15 mammalian cells have transport mechanisms for taking in dsRNA (see, e.g., Asher, et al. (1969) Nature 223:715-717). Consequently, another delivery option is to administer the dsRNA extracellularly into a body cavity, interstitial space or into the blood system of the mammal for subsequent uptake by such transport processes. The blood and lymph systems and the cerebrospinal fluid are potential sites for injecting dsRNA. Oral, topical, parenteral,
20 rectal and intraperitoneal administration are also possible modes of administration.

The composition introduced can also include various other agents in addition to the dsRNA. Examples of such agents include, but are not limited to, those that stabilize the dsRNA, enhance cellular uptake and/or increase the extent of interference. Typically, the dsRNA is introduced in a buffer that is compatible with the composition of the cell into
25 which the RNA is introduced to prevent the cell from being shocked. The minimum size of the dsRNA that effectively achieves gene silencing can also influence the choice of delivery system and solution composition.

Sufficient dsRNA is introduced into the tissue to cause a detectable change in expression of a target gene (assuming the candidate gene is in fact being expressed in the cell
30 into which the dsRNA is introduced) using available detection methodologies. Thus, in some instances, sufficient dsRNA is introduced to achieve at least a 5-10% reduction in candidate gene expression as compared to a cell in which the dsRNA is not introduced. In other instances, inhibition is at least 20, 30, 40 or 50%. In still other instances, the inhibition

is at least 60, 70, 80, 90 or 95%. Expression in some instances is essentially completely inhibited to undetectable levels.

The amount of dsRNA introduced depends upon various factors such as the mode of administration utilized, the size of the dsRNA, the number of cells into which dsRNA is administered, and the age and size of an animal if dsRNA is introduced into an animal. An appropriate amount can be determined by those of ordinary skill in the art by initially administering dsRNA at several different concentrations for example, for example. In certain instances when dsRNA is introduced into a cell culture, the amount of dsRNA introduced into the cells varies from about 0.5 to 3 μg per 10^6 cells.

A number of options are available to detect interference of candidate gene expression (i.e., to detect candidate gene silencing). In general, inhibition in expression is detected by detecting a decrease in the level of the protein encoded by the candidate gene, determining the level of mRNA transcribed from the gene and/or detecting a change in phenotype associated with candidate gene expression.

USE OF POLYPEPTIDES TO SCREEN FOR PEPTIDE ANALOGS AND ANTAGONISTS

Polypeptides encoded by differentially expressed genes identified herein can be used to screen peptide libraries to identify binding partners, such as receptors, from among the encoded polypeptides. Peptide libraries can be synthesized according to methods known in the art (*see, e.g.*, USPN 5,010,175 and WO 91/17823).

Agonists or antagonists of the polypeptides of the invention can be screened using any available method known in the art, such as signal transduction, antibody binding, receptor binding, mitogenic assays, chemotaxis assays, etc. The assay conditions ideally should resemble the conditions under which the native activity is exhibited *in vivo*, that is, under physiologic pH, temperature, and ionic strength. Suitable agonists or antagonists will exhibit strong inhibition or enhancement of the native activity at concentrations that do not cause toxic side effects in the subject. Agonists or antagonists that compete for binding to the native polypeptide can require concentrations equal to or greater than the native concentration, while inhibitors capable of binding irreversibly to the polypeptide can be added in concentrations on the order of the native concentration.

Such screening and experimentation can lead to identification of a polypeptide binding partner, such as a receptor, encoded by a gene or a cDNA corresponding to a polynucleotide described herein, and at least one peptide agonist or antagonist of the binding partner. Such agonists and antagonists can be used to modulate, enhance, or inhibit receptor

function in cells to which the receptor is native, or in cells that possess the receptor as a result of genetic engineering. Further, if the receptor shares biologically important characteristics with a known receptor, information about agonist/antagonist binding can facilitate development of improved agonists/antagonists of the known receptor.

5

VACCINES AND USES

The differentially expressed nucleic acids and polypeptides produced by the nucleic acids of the invention can also be used to modulate primary immune response to prevent or treat cancer. Every immune response is a complex and intricately regulated sequence of events involving several cell types. It is triggered when an antigen enters the body and encounters a specialized class of cells called antigen-presenting cells (APCs). These APCs capture a minute amount of the antigen and display it in a form that can be recognized by antigen-specific helper T lymphocytes. The helper (Th) cells become activated and, in turn, promote the activation of other classes of lymphocytes, such as B cells or cytotoxic T cells. The activated lymphocytes then proliferate and carry out their specific effector functions, which in many cases successfully activate or eliminate the antigen. Thus, activating the immune response to a particular antigen associated with a cancer cell can protect the patient from developing cancer or result in lymphocytes eliminating cancer cells expressing the antigen.

Gene products, including polypeptides, mRNA (particularly mRNAs having distinct secondary and/or tertiary structures), cDNA, or complete gene, can be prepared and used in vaccines for the treatment or prevention of hyperproliferative disorders and cancers. The nucleic acids and polypeptides can be utilized to enhance the immune response, prevent tumor progression, prevent hyperproliferative cell growth, and the like. Methods for selecting nucleic acids and polypeptides that are capable of enhancing the immune response are known in the art. Preferably, the gene products for use in a vaccine are gene products which are present on the surface of a cell and are recognizable by lymphocytes and antibodies.

The gene products may be formulated with pharmaceutically acceptable carriers into pharmaceutical compositions by methods known in the art. The composition is useful as a vaccine to prevent or treat cancer. The composition may further comprise at least one co-immunostimulatory molecule, including but not limited to one or more major histocompatibility complex (MHC) molecules, such as a class I or class II molecule, preferably a class I molecule. The composition may further comprise other stimulator

molecules including B7.1, B7.2, ICAM-1, ICAM-2, LFA-1, LFA-3, CD72 and the like, immunostimulatory polynucleotides (which comprise an 5'-CG-3' wherein the cytosine is unmethylated), and cytokines which include but are not limited to IL-1 through IL-15, TNF- α , IFN- γ , RANTES, G-CSF, M-CSF, IFN- α , CTAP III, ENA-78, GRO, I-309, PF-4, IP-10, LD-78, MGSA, MIP-1 α , MIP-1 β , or combination thereof, and the like for
5 immunopotentialiation. In one embodiment, the immunopotentialiators of particular interest are those that facilitate a Th1 immune response.

The gene products may also be prepared with a carrier that will protect the gene products against rapid elimination from the body, such as a controlled release formulation, including implants and microencapsulated delivery systems. Biodegradable polymers can be
10 used, such as ethylene vinyl acetate, polyanhydrides, polyglycolic acid, collagen, polyorthoesters, polylactic acid, and the like. Methods for preparation of such formulations are known in the art.

In the methods of preventing or treating cancer, the gene products may be administered via one of several routes including but not limited to transdermal, transmucosal, intravenous, intramuscular, subcutaneous, intradermal, intraperitoneal, intrathecal, intrapleural, intrauterine, rectal, vaginal, topical, intratumor, and the like. For transmucosal or transdermal administration, penetrants appropriate to the barrier to be permeated are used in the formulation. Such penetrants are generally known in the art, and
15 include, for example, administration bile salts and fusidic acid derivatives. In addition, detergents may be used to facilitate permeation. Transmucosal administration may be by nasal sprays or suppositories. For oral administration, the gene products are formulated into conventional oral administration form such as capsules, tablets, elixirs and the like.

The gene product is administered to a patient in an amount effective to prevent or treat cancer. In general, it is desirable to provide the patient with a dosage of gene product of at least about 1 pg per Kg body weight, preferably at least about 1 ng per Kg body weight, more preferably at least about 1 μ g or greater per Kg body weight of the recipient. A range of from about 1 ng per Kg body weight to about 100 mg per Kg body weight is preferred although a lower or higher dose may be administered. The dose is effective to prime,
25 stimulate and/or cause the clonal expansion of antigen-specific T lymphocytes, preferably cytotoxic T lymphocytes, which in turn are capable of preventing or treating cancer in the recipient. The dose is administered at least once and may be provided as a bolus or a continuous administration. Multiple administrations of the dose over a period of several weeks to months may be preferable. Subsequent doses may be administered as indicated.

In another method of treatment, autologous cytotoxic lymphocytes or tumor infiltrating lymphocytes may be obtained from a patient with cancer. The lymphocytes are grown in culture, and antigen-specific lymphocytes are expanded by culturing in the presence of the specific gene products alone or in combination with at least one co-immunostimulatory molecule with cytokines. The antigen-specific lymphocytes are then infused back into the patient in an amount effective to reduce or eliminate the tumors in the patient. Cancer vaccines and their uses are further described in USPN 5,961,978; USPN 5,993,829; USPN 6,132,980; and WO 00/38706.

10 PHARMACEUTICAL COMPOSITIONS AND USES

Pharmaceutical compositions can comprise polypeptides, receptors that specifically bind a polypeptide produced by a differentially expressed gene (*e.g.*, antibodies, or polynucleotides (including antisense nucleotides and ribozymes) of the claimed invention in a therapeutically effective amount. The compositions can be used to treat primary tumors as well as metastases of primary tumors. In addition, the pharmaceutical compositions can be used in conjunction with conventional methods of cancer treatment, *e.g.*, to sensitize tumors to radiation or conventional chemotherapy.

Where the pharmaceutical composition comprises a receptor (such as an antibody) that specifically binds to a gene product encoded by a differentially expressed gene, the receptor can be coupled to a drug for delivery to a treatment site or coupled to a detectable label to facilitate imaging of a site comprising breast cancer cells. Methods for coupling antibodies to drugs and detectable labels are well known in the art, as are methods for imaging using detectable labels.

The term "therapeutically effective amount" as used herein refers to an amount of a therapeutic agent to treat, ameliorate, or prevent a desired disease or condition, or to exhibit a detectable therapeutic or preventative effect. The effect can be detected by, for example, chemical markers or antigen levels. Therapeutic effects also include reduction in physical symptoms, such as decreased body temperature.

The precise effective amount for a subject will depend upon the subject's size and health, the nature and extent of the condition, and the therapeutics or combination of therapeutics selected for administration. Thus, it is not useful to specify an exact effective amount in advance. However, the effective amount for a given situation is determined by routine experimentation and is within the judgment of the clinician. For purposes of the present invention, an effective dose will generally be from about 0.01 mg/kg to 50 mg/kg or

0.05 mg/kg to about 10 mg/kg of the DNA constructs in the individual to which it is administered.

A pharmaceutical composition can also contain a pharmaceutically acceptable carrier. The term "pharmaceutically acceptable carrier" refers to a carrier for administration of a therapeutic agent, such as antibodies or a polypeptide, genes, and other therapeutic agents. The term refers to any pharmaceutical carrier that does not itself induce the production of antibodies harmful to the individual receiving the composition, and which can be administered without undue toxicity. Suitable carriers can be large, slowly metabolized macromolecules such as proteins, polysaccharides, polylactic acids, polyglycolic acids, polymeric amino acids, amino acid copolymers, lipid aggregates and inactive virus particles. Such carriers are well known to those of ordinary skill in the art. Pharmaceutically acceptable carriers in therapeutic compositions can include liquids such as water, saline, glycerol and ethanol. Auxiliary substances, such as wetting or emulsifying agents, pH buffering substances, and the like, can also be present in such vehicles.

Typically, the therapeutic compositions are prepared as injectables, either as liquid solutions or suspensions; solid forms suitable for solution in, or suspension in, liquid vehicles prior to injection can also be prepared. Liposomes are included within the definition of a pharmaceutically acceptable carrier. Pharmaceutically acceptable salts can also be present in the pharmaceutical composition, e.g., mineral acid salts such as hydrochlorides, hydrobromides, phosphates, sulfates, and the like; and the salts of organic acids such as acetates, propionates, malonates, benzoates, and the like. A thorough discussion of pharmaceutically acceptable excipients is available in *Remington: The Science and Practice of Pharmacy* (1995) Alfonso Gennaro, Lippincott, Williams, & Wilkins.

DELIVERY METHODS

Once formulated, the compositions contemplated by the invention can be (1) administered directly to the subject (e.g., as polynucleotide, polypeptides, small molecule agonists or antagonists, and the like); or (2) delivered ex vivo, to cells derived from the subject (e.g., as in *ex vivo* gene therapy). Direct delivery of the compositions will generally be accomplished by parenteral injection, e.g., subcutaneously, intraperitoneally, intravenously or intramuscularly, intratumoral or to the interstitial space of a tissue. Other modes of administration include oral and pulmonary administration, suppositories, and transdermal applications, needles, and gene guns or hyposprays. Dosage treatment can be a single dose schedule or a multiple dose schedule.

Methods for the ex vivo delivery and reimplantation of transformed cells into a subject are known in the art and described in *e.g.*, International Publication No. WO 93/14778. Examples of cells useful in ex vivo applications include, for example, stem cells, particularly hematopoietic, lymph cells, macrophages, dendritic cells, or tumor cells.

5 Generally, delivery of nucleic acids for both ex vivo and in vitro applications can be accomplished by, for example, dextran-mediated transfection, calcium phosphate precipitation, polybrene mediated transfection, protoplast fusion, electroporation, encapsulation of the polynucleotide(s) in liposomes, and direct microinjection of the DNA into nuclei, all well known in the art.

10 Once differential expression of a gene corresponding to a polynucleotide described herein has been found to correlate with a proliferative disorder, such as neoplasia, dysplasia, and hyperplasia, the disorder can be amenable to treatment by administration of a therapeutic agent based on the provided polynucleotide, corresponding polypeptide or other corresponding molecule (*e.g.*, antisense, ribozyme, etc.). In other embodiments, the disorder
15 can be amenable to treatment by administration of a small molecule drug that, for example, serves as an inhibitor (antagonist) of the function of the encoded gene product of a gene having increased expression in cancerous cells relative to normal cells or as an agonist for gene products that are decreased in expression in cancerous cells (*e.g.*, to promote the activity of gene products that act as tumor suppressors).

20 The dose and the means of administration of the inventive pharmaceutical compositions are determined based on the specific qualities of the therapeutic composition, the condition, age, and weight of the patient, the progression of the disease, and other relevant factors. For example, administration of polynucleotide therapeutic composition agents includes local or systemic administration, including injection, oral administration,
25 particle gun or catheterized administration, and topical administration. In general, the therapeutic polynucleotide composition contains an expression construct comprising a promoter operably linked to a polynucleotide of at least 12, 22, 25, 30, or 35 contiguous nt of the polynucleotide disclosed herein. Various methods can be used to administer the therapeutic composition directly to a specific site in the body. For example, a small
30 metastatic lesion is located and the therapeutic composition injected several times in several different locations within the body of the tumor. Alternatively, arteries which serve a tumor are identified, and the therapeutic composition injected into such an artery, in order to deliver the composition directly into the tumor. A tumor that has a necrotic center is aspirated and the composition injected directly into the now empty center of the tumor. The

antisense composition is directly administered to the surface of the tumor, for example, by topical application of the composition. X-ray imaging is used to assist in certain of the above delivery methods.

Targeted delivery of therapeutic compositions containing an antisense
5 polynucleotide, subgenomic polynucleotides, or antibodies to specific tissues can also be used. Receptor-mediated DNA delivery techniques are described in, for example, Findeis et al., Trends Biotechnol. (1993) 11:202; Chiou et al., Gene Therapeutics: Methods And Applications Of Direct Gene Transfer (J.A. Wolff, ed.) (1994); Wu et al., J. Biol. Chem. (1988) 263:621; Wu et al., J. Biol. Chem. (1994) 269:542; Zenke et al., Proc. Natl. Acad.
10 Sci. (USA) (1990) 87:3655; Wu et al., J. Biol. Chem. (1991) 266:338. Therapeutic compositions containing a polynucleotide are administered in a range of about 100 ng to about 200 mg of DNA for local administration in a gene therapy protocol. Concentration ranges of about 500 ng to about 50 mg, about 1 μ g to about 2 mg, about 5 μ g to about 500 μ g, and about 20 μ g to about 100 μ g of DNA can also be used during a gene therapy
15 protocol. Factors such as method of action (e.g., for enhancing or inhibiting levels of the encoded gene product) and efficacy of transformation and expression are considerations that will affect the dosage required for ultimate efficacy of the antisense subgenomic polynucleotides.

Where greater expression is desired over a larger area of tissue, larger amounts of
20 antisense subgenomic polynucleotides or the same amounts readministered in a successive protocol of administrations, or several administrations to different adjacent or close tissue portions of, for example, a tumor site, may be required to effect a positive therapeutic outcome. In all cases, routine experimentation in clinical trials will determine specific ranges for optimal therapeutic effect. For polynucleotide related genes encoding
25 polypeptides or proteins with anti-inflammatory activity, suitable use, doses, and administration are described in USPN 5,654,173.

The therapeutic polynucleotides and polypeptides of the present invention can be delivered using gene delivery vehicles. The gene delivery vehicle can be of viral or non-viral origin (see generally, Jolly, Cancer Gene Therapy (1994) 1:51; Kimura, Human Gene
30 Therapy (1994) 5:845; Connelly, Human Gene Therapy (1995) 1:185; and Kaplitt, Nature Genetics (1994) 6:148). Expression of such coding sequences can be induced using endogenous mammalian or heterologous promoters. Expression of the coding sequence can be either constitutive or regulated.

Viral-based vectors for delivery of a desired polynucleotide and expression in a desired cell are well known in the art. Exemplary viral-based vehicles include, but are not limited to, recombinant retroviruses (see, e.g., WO 90/07936; WO 94/03622; WO 93/25698; WO 93/25234; USPN 5, 219,740; WO 93/11230; WO 93/10218; USPN 4,777,127; GB
5 Patent No. 2,200,651; EP 0 345 242; and WO 91/02805), alphavirus-based vectors (e.g., Sindbis virus vectors, Semliki forest virus (ATCC VR-67; ATCC VR-1247), Ross River virus (ATCC VR-373; ATCC VR-1246) and Venezuelan equine encephalitis virus (ATCC VR-923; ATCC VR-1250; ATCC VR 1249; ATCC VR-532), and adeno-associated virus (AAV) vectors (see, e.g., WO 94/12649, WO 93/03769; WO 93/19191; WO 94/28938;
10 WO 95/11984 and WO 95/00655). Administration of DNA linked to killed adenovirus as described in Curiel, Hum. Gene Ther. (1992) 3:147 can also be employed.

Non-viral delivery vehicles and methods can also be employed, including, but not limited to, polycationic condensed DNA linked or unlinked to killed adenovirus alone (see, e.g., Curiel, Hum. Gene Ther. (1992) 3:147); ligand-linked DNA (see, e.g., Wu, J. Biol.
15 Chem. (1989) 264:16985); eukaryotic cell delivery vehicles cells (see, e.g., USPN 5,814,482; WO 95/07994; WO 96/17072; WO 95/30763; and WO 97/42338) and nucleic charge neutralization or fusion with cell membranes. Naked DNA can also be employed. Exemplary naked DNA introduction methods are described in WO 90/11092 and USPN
20 5,422,120; WO 95/13796; WO 94/23697; WO 91/14445; and EP 0524968. Additional approaches are described in Philip, *Mol. Cell Biol.* (1994) 14:2411, and in Woffendin, *Proc. Natl. Acad. Sci.* (1994) 91:1581.

Further non-viral delivery suitable for use includes mechanical delivery systems such as the approach described in Woffendin *et al.*, *Proc. Natl. Acad. Sci. USA* (1994)
25 91(24):11581. Moreover, the coding sequence and the product of expression of such can be delivered through deposition of photopolymerized hydrogel materials or use of ionizing radiation (see, e.g., USPN 5,206,152 and WO 92/11033). Other conventional methods for gene delivery that can be used for delivery of the coding sequence include, for example, use of hand-held gene transfer particle gun (see, e.g., USPN 5,149,655); use of ionizing radiation
30 for activating transferred gene (see, e.g., USPN 5,206,152 and WO 92/11033).

EXAMPLES

The following examples are put forth so as to provide those of ordinary skill in the art with a complete disclosure and description of how to make and use the present invention,

and are not intended to limit the scope of what the inventors regard as their invention nor are they intended to represent that the experiments below are all or the only experiments performed. Efforts have been made to ensure accuracy with respect to numbers used (e.g. amounts, temperature, etc.) but some experimental errors and deviations should be accounted for. Unless indicated otherwise, parts are parts by weight, molecular weight is weight average molecular weight, temperature is in degrees Centigrade, and pressure is at or near atmospheric.

EXAMPLE 1:

SOURCE OF BIOLOGICAL MATERIALS

10 The cells used for detecting differential expression of breast cancer related genes were those previously described for the HMT-3522 tumor reversion model, disclosed in U.S. Patent Nos. 5,846,536 and 6,123,941, herein incorporated by reference. The model utilizes both non-tumorigenic (HMT-3522 S1) and tumorigenic (HMT-3522 T4-2) cells derived by serial passaging from a single reduction mammoplasty. In two dimensional (2D)
15 monolayers on plastic, both S1 and T4-2 cells display similar morphology. But in three dimensional (3D) matrigel cultures, S1 form phenotypically normal mammary tissue structures while T4-2 cells fail to organize into these structures and instead disseminate into the matrix. This assay was designated as a tumor reversion model, in that the T4-2 cells can be induced to form S1-like structures in 3D by treatment with beta-1 integrin or EGFR
20 blocking antibodies, or by treating with a chemical inhibitor of the EGFR signaling pathway (tyrophostin AG 1478). These treated T4-2 cells, called T4R cells, are non-tumorigenic.

EXAMPLE 2:

CELL GROWTH AND RNA ISOLATION

Growth of Cells 2D and 3D for Microarray Experiments: HMT3522 S1 and T4-2
25 cells were grown 2D and 3D and T4-2 cells reverted with anti-EGFR, anti-beta 1 integrin, or tyrophostin AG 1478 as previously described (Weaver et al J Cell Biol. 137:231-45, 1997; and Wang et al PNAS 95:14821-14826, 1998). Anti-EGFR (mAb 225) was purchased from Oncogene and introduced into the matrigel at the time of gelation at a concentration of 4 ug/ml purified mouse IgG1. Anti-beta 1 integrin (mAb AIIB2) was a gift from C. Damsky
30 at the University of California at San Francisco and was also introduced into the matrigel at the time of gelation at a concentration of 100 ug/ml ascites protein (which corresponds to 4-10 ug/ml purified rat IgG1). Tyrophostin AG 1478 was purchased from Calbiochem and used at a concentration of 100 nM.

Isolation of RNA for Microarray Experiments: RNA was prepared from: S1 passage 60 2D cultures; T4-2 passage 41 2D cultures; S1 passage 59 3D cultures; and T4-2 and T4-2 revertant (with anti-EGFR, anti-beta 1 integrin, and tyrophostin) passage 35 3D cultures.

5 All RNA for microarray experiments was isolated using the commercially available RNeasy Mini Kit from Qiagen. Isolation of total RNA from cells grown 2D was performed as instructed in the kit handbook. Briefly, media was aspirated from the cells and kit Buffer RLT was added directly to the flask. The cell lysate was collected with a rubber cell scraper, and the lysate passed 5 times through a 20-G needle fitted to a syringe. One volume of 70% ethanol was added to the homogenized lysate and mixed well by pipetting. Up to 700 ul of sample was applied to an RNeasy mini spin column sitting in a 2-ml collection tube and
10 centrifuged for 15 seconds at >8000 x g. 700 ul Buffer RW1 was added to the column and centrifuged for 15 seconds at >8000 x g to wash. The column was transferred to a new collection tube. 500 ul Buffer RPE was added to the column and centrifuged for 15 seconds at >8000 x g to wash. Another 500 ul Buffer RPE was added to the column for additional
15 washing, and the column centrifuged for 2 minutes at maximum speed to dry. The column was transferred to a new collection tube and RNA eluted from the column with 30 ul RNase-free water by centrifuging for 1 minute at >8000 x g.

Isolation of total RNA from cells grown 3D was performed as described above, except cells were isolated from matrigel prior to RNA isolation. The cells were isolated as
20 colonies from matrigel using ice-cold PBS/EDTA (0.01 M sodium phosphate pH 7.2 containing 138 mM sodium chloride and 5 mM EDTA). See Weaver et al, J Cell Biol 137:231-245, 1997; and Wang et al. PNAS 95:14821-14826, 1998.

EXAMPLE 3:

DETECTION AND IDENTIFICATION OF GENES EXHIBITING DIFFERENTIAL EXPRESSION

25 The relative expression levels of a selected sequence (which in turn is representative of a single transcript) were examined in the tumorigenic versus non-tumorigenic cell lines described above, following culturing of the cells (S1, T4-2 and T4R) in either two-dimensional (2D) monolayers or three-dimensional (3D) matrigel cultures as described above. Differential expression for a selected sequence was assessed by hybridizing mRNA
30 from S1 and T4-2 2D cultures, and S1, T4-2 and T4R 3D cultures to microarray chips as described below, as follows: Exp1 = T4-2 2D/S1 2D; Exp2 = T4-2 3D/S1 3D; Exp3 = S1 3D/S1 2D; Exp4 = T4-2 3D/T4-2 2D; Exp5 = T4-2 3D/T4R (anti-EGFR) 3D; Exp6 = T4-2 3D/T4R (anti-beta1 integrin) 3D; and Exp7 = T4-2 3D/T4R (tyrophostin AG 1478) 3D.

Each array used had an identical spatial layout and control spot set. Each microarray was divided into two areas, each area having an array with, on each half, twelve groupings of 32 x 12 spots for a total of about 9,216 spots on each array. The two areas are spotted identically which provide for at least two duplicates of each clone per array. Spotting was accomplished using PCR amplified products from 0.5kb to 2.0 kb and spotted using a Molecular Dynamics Gen III spotter according to the manufacturer's recommendations. The first row of each of the 24 regions on the array had about 32 control spots, including 4 negative control spots and 8 test polynucleotides.

The test polynucleotides were spiked into each sample before the labeling reaction with a range of concentrations from 2-600 pg/slide and ratios of 1:1. For each array design, two slides were hybridized with the test samples reverse-labeled in the labeling reaction. This provided for about 4 duplicate measurements for each clone, two of one color and two of the other, for each sample.

Identification Of Differentially Expressed Genes: "Differentially expressed" in the context of the present example meant that there was a difference in expression of a particular gene between tumorigenic vs. non-tumorigenic cells, or cells grown in three-dimensional culture vs. cells grown in two-dimensional culture. To identify differentially expressed genes, total RNA was first reverse transcribed into cDNA using a primer containing a T7 RNA polymerase promoter, followed by second strand DNA synthesis. cDNA was then transcribed *in vitro* to produce antisense RNA using the T7 promoter-mediated expression (see, e.g., Luo *et al.* (1999) *Nature Med* 5:117-122), and the antisense RNA was then converted into cDNA. The second set of cDNAs were again transcribed *in vitro*, using the T7 promoter, to provide antisense RNA. Optionally, the RNA was again converted into cDNA, allowing for up to a third round of T7-mediated amplification to produce more antisense RNA. Thus the procedure provided for two or three rounds of *in vitro* transcription to produce the final RNA used for fluorescent labeling.

Fluorescent probes were generated by first adding control RNA to the antisense RNA mix, and producing fluorescently labeled cDNA from the RNA starting material. Fluorescently labeled cDNAs prepared from tumorigenic RNA sample were compared to fluorescently labeled cDNAs prepared from non-tumorigenic cell RNA sample. For example, the cDNA probes from the non-tumorigenic cells were labeled with Cy3 fluorescent dye (green) and the cDNA probes prepared from the tumorigenic cells were labeled with Cy5 fluorescent dye (red).

The differential expression assay was performed by mixing equal amounts of probes from tumorigenic cells and non-tumorigenic cells, and/or cells grown in 3D vs. those grown in 2D. The arrays were prehybridized by incubation for about 2 hrs at 60°C in 5X SSC/0.2% SDS/1 mM EDTA, and then washed three times in water and twice in isopropanol.

- 5 Following prehybridization of the array, the probe mixture was then hybridized to the array under conditions of high stringency (overnight at 42°C in 50% formamide, 5X SSC, and 0.2% SDS). After hybridization, the array was washed at 55°C three times as follows: 1) first wash in 1X SSC/0.2% SDS; 2) second wash in 0.1X SSC/0.2% SDS; and 3) third wash in 0.1X SSC.

- 10 The arrays were then scanned for green and red fluorescence using a Molecular Dynamics Generation III dual color laser-scanner/detector. The images were processed using BioDiscovery Autogene software, and the data from each scan set normalized to provide for a ratio of expression relative to non-tumorigenic or tumorigenic cells grown two-dimensionally or three-dimensionally. Data from the microarray experiments was analyzed
15 according to the algorithms described in U.S. application serial no. 60/252,358, filed November 20, 2000, by E.J. Moler, M.A. Boyle, and F.M. Randazzo, and entitled "Precision and accuracy in cDNA microarray data," which application is specifically incorporated herein by reference.

- The experiment was repeated, this time labeling the two probes with the opposite
20 color in order to perform the assay in both "color directions." Each experiment was sometimes repeated with two more slides (one in each color direction). The level of fluorescence for each sequence on the array expressed as a ratio of the geometric mean of 8 replicate spots/genes from the four arrays or 4 replicate spots/gene from 2 arrays or some other permutation. The data were normalized using the spiked positive controls present in
25 each duplicated area, and the precision of this normalization was included in the final determination of the significance of each differential. The fluorescence intensity of each spot was also compared to the negative controls in each duplicated area to determine which spots have detected significant expression levels in each sample.

- A statistical analysis of the fluorescent intensities was applied to each set of duplicate
30 spots to assess the precision and significance of each differential measurement, resulting in a p-value testing the null hypothesis that there is no differential in the expression level between the tumorigenic and non-tumorigenic cells or cells grown two-dimensionally versus three-dimensionally. During initial analysis of the microarrays, the hypothesis was accepted if $p > 10^{-3}$, and the differential ratio was set to 1.000 for those spots. All other spots have a

significant difference in expression between the two samples compared. For example, if the tumorigenic sample has detectable expression and the non-tumorigenic does not, the ratio is truncated at 1000 since the value for expression in the non-tumorigenic sample would be zero, and the ratio would not be a mathematically useful value (e.g., infinity). If the non-tumorigenic sample has detectable expression and the tumorigenic does not, the ratio is truncated to 0.001, since the value for expression in the tumor sample would be zero and the ratio would not be a mathematically useful value. These latter two situations are referred to herein as "on/off." Database tables were populated using a 95% confidence level ($p > 0.05$).

In general, a polynucleotide is said to represent a significantly differentially expressed gene between two samples when there is detectable levels of expression in at least one sample and the ratio value is greater than at least about 1.2 fold, at least about 1.5 fold, or at least about 2 fold, where the ratio value is calculated using the method described above.

A differential expression ratio of 1 indicates that the expression level of the gene in tumorigenic cells was not statistically different from expression of that gene in the specific non-tumorigenic cells compared. A differential expression ratio significantly greater than 1 in tumorigenic breast cells relative to non-tumorigenic breast cells indicates that the gene is increased in expression in tumorigenic cells relative to non-tumorigenic cells, suggesting that the gene plays a role in the development of the tumorigenic phenotype, and may be involved in promoting metastasis of the cell. Detection of gene products from such genes can provide an indicator that the cell is cancerous, and may provide a therapeutic and/or diagnostic target. Likewise, a differential expression ratio significantly less than 1 in tumorigenic breast cells relative to non-tumorigenic breast cells indicates that, for example, the gene is involved in suppression of the tumorigenic phenotype. Increasing activity of the gene product encoded by such a gene, or replacing such activity, can provide the basis for chemotherapy. Such gene can also serve as markers of cancerous cells, e.g., the absence or decreased presence of the gene product in a breast cell relative to a non-tumorigenic breast cell indicates that the cell is cancerous.

Using the above methodology, three hundred and sixty-seven (367) genes or products thereof were identified from 20,000 chip clones analyzed as being overexpressed 2-fold or more in one or more of these experiments, with a p-value of 0.001 or less. These identified genes or products thereof are listed in Table 1, according to the Spot ID of the spotted polynucleotide, the Sample ID, the corresponding GenBank Accession Number (No.), the GenBank description (if available) for the corresponding Genbank Accession Number, and

the GenBank score (p-value; the probability that the association between the SEQ ID NO. and the gene or product thereof occurred by chance). The polynucleotide and polypeptide sequences, as provided by any disclosed Genbank entries are herein incorporated by reference to the corresponding Genbank accession number. The differential hybridization results from the seven differential expression microarray experiments listed above are provided in Table 2, where sequences have a measurement corresponding to its ratio of expression in the 7 experiments, e.g. spot ID 10594 is 2.2-fold overexpressed in 3D T4-2 cells as compared to 3D S1 cells. SEQ ID NOS:1-499, representing the sequences corresponding to the spot Ids listed in Tables 1 and 2 are provided in the sequence listing. Table 11 is a lookup table showing the relationship between the spot Ids (i.e. the nucleic acids spotted on the microarray) and the sequences provided in the sequence listing.

EXAMPLE 4

CYCLIN G ASSOCIATED KINASE (GAK)

A gene or product thereof called cyclin G associated kinase, or GAK, was identified as being overexpressed in 3D T4-2 cultures relative to both 3D S1 cultures (ratio: 7.9296) and 2D T4-2 cultures (ratio: 34.6682) (Sample ID RG:1056692:10012:C11, Spot ID 19990). GAK corresponds to Genbank Accession number XM_003450.

EXAMPLE 5

ANTISENSE REGULATION OF GAK EXPRESSION

Additional functional information on GAK was generated using antisense knockout technology. A number of different oligonucleotides complementary to GAK mRNA were designed (AS) with corresponding controls (RC): GGAATCACCGCTTTGCCATCTTCAA (SEQ ID NO:500; CHIR159-1AS, gak:P1868AS), AACTTCTACCGTTTCGCCACTAAGG (SEQ ID NO:501; CHIR159-1RC, gak:P1868RC); GACCGTGTA CTGCGTGTCGTGCG (SEQ ID NO:502; CHIR159-7AS, gak:P0839AS) and GCGTGCTGTGCGTCATGTGCCAG (SEQ ID NO:502; CHIR159-7RC, gak:P0839RC), and tested for their ability to suppress expression of GAK in human malignant colorectal carcinoma SW620 cells, human breast cancer MDA231 cells, and human breast cancer T4-2 cells. For each transfection mixture, a carrier molecule, preferably a lipitoid or cholesterol, was prepared to a working concentration of 0.5 mM in water, sonicated to yield a uniform solution, and filtered through a 0.45 μ m PVDF membrane. The antisense or control oligonucleotide was then prepared to a working concentration of 100 μ M in sterile Millipore water. The oligonucleotide was further diluted in OptiMEM™ (Gibco/BRL), in a microfuge

tube, to 2 μ M, or approximately 20 μ g oligo/ml of OptiMEM™. In a separate microfuge tube, lipitoid or cholesterol, typically in the amount of about 1.5-2 nmol lipitoid/ μ g antisense oligonucleotide, was diluted into the same volume of OptiMEM™ used to dilute the oligonucleotide. The diluted antisense oligonucleotide was immediately added to the
5 diluted lipitoid and mixed by pipetting up and down. Oligonucleotide was added to the cells to a final concentration of 300 nM.

The level of target mRNA (GAK) in the transfected cells was quantitated in the cancer cell lines using the methods using primers CHIR159_2896 (GCCGTCTTCAGGCAACAACCTCCCA; SEQ ID NO: 504; forward) and CHIR159_3089
10 (TGCTGGACGAGGCTGTCATCTTGC; SEQ ID NO:505; reverse). RNA was extracted as above according to manufacturer's directions.

Quantitative PCR (qPCR) was performed by first isolating the RNA from the above mentioned tissue/cells using a Qiagen RNeasy mini prep kit. A total of 0.5 micrograms of RNA was used to generate a first strand cDNA using Stratagene MuLV Reverse
15 Transcriptase, using recommended concentrations of buffer, enzyme, and Rnasin. Concentrations and volumes of dNTP, and oligo dT, or random hexamers were lower than recommended to reduce the level of background primer dimerization in the qPCR.

The cDNA is then used for qPCR to determine the levels of expression of GAK using the GeneAmp 7000 by ABI as recommended by the manufacturer. Primers for actin were
20 also used in order to normalized the values, and eliminate possible variations in cDNA template concentrations, pipetting error, etc.

For each 20 μ l reaction, extracted RNA (generally 0.2-1 μ g total) was placed into a sterile 0.5 or 1.5 ml microcentrifuge tube, and water was added to a total volume of 12.5 μ l. To each tube was added 7.5 μ l of a buffer/enzyme mixture, prepared by mixing (in the order
25 listed) 2.5 μ l H₂O, 2.0 μ l 10X reaction buffer, 10 μ l oligo dT (20 pmol), 1.0 μ l dNTP mix (10 mM each), 0.5 μ l RNAsin® (20u) (Ambion, Inc., Hialeah, FL), and 0.5 μ l MMLV reverse transcriptase (50u) (Ambion, Inc.). The contents were mixed by pipetting up and down, and the reaction mixture was incubated at 42°C for 1 hour. The contents of each tube were centrifuged prior to amplification.

30 An amplification mixture was prepared by mixing in the following order: 1X PCR buffer II, 3 mM MgCl₂, 140 μ M each dNTP, 0.175 pmol each oligo, 1:50,000 dil of SYBR® Green, 0.25 mg/ml BSA, 1 unit *Taq* polymerase, and H₂O to 20 μ l. (PCR buffer II is available in 10X concentration from Perkin-Elmer, Norwalk, CT). In 1X concentration it contains 10 mM Tris pH 8.3 and 50 mM KCl. SYBR® Green (Molecular Probes, Eugene,

OR) is a dye which fluoresces when bound to double stranded DNA. As double stranded PCR product is produced during amplification, the fluorescence from SYBR® Green increases. To each 20 µl aliquot of amplification mixture, 2 µl of template RT was added, and amplification was carried out according to standard protocols.

- 5 Table 3 shows that the antisense oligonucleotides described above reduced expression of GAK mRNA as compared to controls in all three cell lines. GAK mRNA reduction ranged from about 50% to about 90%, as compared to cells transfected with reverse (i.e. sense) control oligonucleotides.

Table 3: antisense regulation of GAK mRNA

Oligo	Cell Line	Gene Message	Actin Message	Ratio	Percent KO
CHIR159-1AS	SW620	0.0923	0.669	0.138	90.7
CHIR159-1RC	SW620	1.01	0.680	1.49	
CHIR159-7AS	SW620	0.0555	0.678	0.082	85.4
CHIR159-7RC	SW620	0.335	0.598	0.560	
CHIR159-1AS	MDA231	0.358	0.687	0.521	59.3
CHIR159-1RC	MDA231	1.00	0.784	1.28	
CHIR159-7AS	MDA231	0.262	0.674	0.389	69.4
CHIR159-7RC	MDA231	0.840	0.659	1.27	
CHIR159-1AS	T4-2	0.307	0.707	0.434	72.9
CHIR159-1RC	T4-2	1.23	0.770	1.60	
CHIR159-7AS	T4-2	0.214	0.649	0.330	49.8
CHIR159-7RC	T4-2	0.506	0.770	0.657	

10

Reduction of GAK protein by antisense polynucleotides in SW620, MDA231 and T4-2 was confirmed using an antibody that specifically recognizes GAK. Figure 1 shows a western (i.e. protein) blot of protein extracts of the above cell lines decorated with anti-GAK antibodies. GAK protein expression is reduced in cell lines receiving GAK antisense
 15 oligonucleotides.

EXAMPLE 6

ROLE OF GAK IN ANCHORAGE INDEPENDENT CELL GROWTH

The effect of GAK gene expression upon anchorage-independent cell growth of SW620 and MBA-231 cells was measured by colony formation in soft agar. Soft agar assays were performed by first coating a non-tissue culture treated plate with PolyHEMA to prevent cells from attaching to the plate. Non-transfected cells were harvested using 0.05% trypsin and washing twice in media. The cells are counted using a hemacytometer and resuspended to 10^4 per ml in media. 50 μ l aliquots are placed in poly-HEMA coated 96-well plates and transfected. For each transfection mixture, a carrier molecule, preferably a lipitoid or cholesterol, was prepared to a working concentration of 0.5 mM in water, sonicated to yield a uniform solution, and filtered through a 0.45 μ m PVDF membrane. The antisense or control oligonucleotide was then prepared to a working concentration of 100 μ M in sterile Millipore water. The oligonucleotide was further diluted in OptiMEM™ (Gibco/BRL), in a microfuge tube, to 2 μ M, or approximately 20 μ g oligo/ml of OptiMEM™. In a separate microfuge tube, lipitoid or cholesterol, typically in the amount of about 1.5-2 nmol lipitoid/ μ g antisense oligonucleotide, was diluted into the same volume of OptiMEM™ used to dilute the oligonucleotide. The diluted antisense oligonucleotide was immediately added to the diluted lipitoid and mixed by pipetting up and down. Oligonucleotide was added to the cells to a final concentration of 300 nM. Following transfection (~30 minutes), 3% GTG agarose is added to the cells for a final concentration of 0.35% agarose. After the cell layer agar solidifies, 100 μ l of media is dribbled on top of each well. Colonies form in 7 days. For a read-out of growth, 20 μ l of Alamar Blue is added to each well and the plate is shaken for 15 minutes. Fluorecence readings (530nm excitation 590 nm emission) are taken after incubation for 6-24 hours.

The data presented in Table 4 shows that the application of GAK antisense oligonucleotides to SW620 and MDA 231 cells results in inhibition of colony formation and shows that GAK plays a role in production anchorage-independent cell growth. Table 4 shows the average fluorescence reading for several experiments. The standard deviation (St. Dev) of the fluorescence reading and coefficient of variation (%CV) is also shown.

Table 4: GAK and anchorage-independent cell growth.

Oligo	Cell Line	Average	St. Dev	%CV
Blank	SW620	12868.17	208.78	1.78
Untreated	SW620	31075.17	1944.36	7.66
Pos Control	SW620	5717.17	1108.71	23.75
Neg Control	SW620	7576.17	465.95	7.63
Chir159-1AS	SW620	9701.5	2281.36	28.8
Chir159-1RC	SW620	17765.5	1958.45	13.5
Blank	MDA231	12726.83	232.45	2
Untreated	MDA231	87272.17	0	0
Pos Control	MDA231	10645.17	1591.08	18.31
Neg Control	MDA231	24159.5	2850.58	14.45
Chir159-1AS	MDA231	8613.5	4852.76	69
Chir159-1RC	MDA231	17859.17	1535.55	10.53

EXAMPLE 7

DKFZp566I133 (DKFZ)

Several previously uncharacterized genes were identified as being induced in these experiments. One such gene was represented by two spots, Spot ID Nos 22793 and 26883 (gene assignment DKFZp566I133). This gene was expressed at a ratio of about 2.2 in two 2-dimensional (2D) T4-2 vs. 2D S1 experiments, and also at a ratio of about 2 when 3-dimensional (3D) T4-2 cells were compared to the various tumor reversion cultures. However, the ratio of expression increased to an average of 3.2 when 3-dimensional (3D) T4-2 cultures were compared to 2D S1 cultures. In contrast, there was essentially no difference in expression levels when 3D S1 cultures were compared to 2D S1 cultures, suggesting that expression of this gene is specifically elevated in the tumorigenic cell line T4-2, and even further elevated when the tumorigenic cell line is grown in three dimensional cultures (see Table 5).

Table 5.

Spot	2D T4-2/	3D T42/	3D S1/	3D T4-2/	3D T4-2/	3D T4-2/	3D T4-2/
ID	2D S1	3D S1	2D S1	2D T4-2	EGFRAb	B1 integrin	Tyr
22893	1.90387	2.64711	0.522161	1	2.17956	1.75287	2.055538
26883	2.43428	3.74613	0.524466	1	2.467573	2.029468	2.002817

These array data were confirmed by qPCR using the methods described above and the gene specific PCR primers CHIR180_1207 ACAGGGAGAAAAGTGGTTGTCCTGG (SEQ ID NO:506; Forward) and CHIR180_1403 AAGGCAGAACCCATCCACTCCAA (SEQ ID NO:507; Reverse). Independent cultures were used for these experiments, and data was normalized to B-catenin. These data are shown in Table 6.

Table 6.

2D S1	2D T4-2	3D S1	3D T4-2	3D EGFRAb	3D B1 Integrin	3D Tyr
0.165	0.421	0.14	0.475	0.231	0.175	0.174

DKFZ corresponds to Genbank Accession numbers NP_112200, AAH09758, and NM_030938. Orthologs of DKFZ are identified in species other than Homo sapiens include NM_138839 from *Rattus norvegicus*.

Analysis of the sequence of DKFZ using a transmembrane helix prediction algorithm (Sonhammer, et al, A hidden Markov model for predicting transmembrane helices in protein sequences, In Proc. of Sixth Int. Conf. on Intelligent Systems for Molecular Biology, p. 175-82, Ed. J. Glasgow, T. Littlejohn, F. Major, R. Lathrop, D. Sankoff, and C. Sensen, Menlo Park, CA: AAAI Press, 1998) indicates that the DKFZ protein has six transmembrane regions (Fig.2), and, as such, is likely to be a transmembrane protein.

EXAMPLE 8

ANTISENSE REGULATION OF DKFZ EXPRESSION

Additional functional information on DKFZ was generated using antisense knockout technology. A number of different oligonucleotides complementary to DKFZ mRNA were designed (AS) with corresponding controls (RC): GCTGCTGGATTCGTTTGGCATAACT (SEQ ID NO: 508; CHIR180-7AS, DKFZp56611:P1301AS),

- TCAATACGGTTTGCTTAGGTCGTCG (SEQ ID NO:509; CHIR180-7RC, DKFZp566I1:P1301RC), TCTCCTCTGAGTTCAACCGCTGCT (SEQ ID NO:510; CHIR180-8AS, DKFZp566I1:P1320AS) and TCGTCGCCAACTTGAGTCTCCTCT (SEQ ID NO:511; CHIR180-8RC, DKFZp566I1:P1320AS), and tested for their ability to suppress
- 5 expression of DKFZ in human malignant colorectal carcinoma SW620 cells, human breast cancer MDA231 cells, and human breast cancer T4-2 cells, as described above.

Table 7 shows that the antisense (AS) oligonucleotides described above reduced expression of DKFZ mRNA as compared to controls in all three cell lines. DKFZ mRNA reduction ranged from about 95% to about 99%, as compared to cells transfected with

10 reverse (i.e. sense) control (RC) oligonucleotides.

Table 7: antisense regulation of DKFZ mRNA

Oligo	Cell Line	Gene Message	Actin Message	Ratio	Percent KO
CHIR180-7AS	SW620	0.0157	0.772	0.020	99.3
CHIR180-7RC	SW620	1.99	0.736	2.70	
CHIR180-8AS	SW620	0.0387	0.681	0.057	97.9
CHIR180-8RC	SW620	1.89	0.703	2.69	
CHIR180-7AS	MDA231	0.0471	3.58	0.013	98.5
CHIR180-7RC	MDA231	1.99	2.33	0.854	
CHIR180-8AS	MDA231	0.00935	1.74	0.00537	99.5
CHIR180-8RC	MDA231	1.14	1.01	1.13	
CHIR180-7AS	T4-2	0.119	0.667	0.178	95.4
CHIR180-7RC	T4-2	2.8	0.728	3.85	
CHIR180-8AS	T4-2	0.0852	0.751	0.113	95.6
CHIR180-8RC	T4-2	1.6	0.620	2.58	

EXAMPLE 9

EFFECT OF DKFZ EXPRESSION ON CELL PROLIFERATION

The effect of gene expression on the inhibition of cell proliferation was assessed in metastatic breast cancer cell line MDA-231 and breast cancer cell line T4-2.

5 Cells were plated to approximately 60-80% confluency in 96-well dishes. Antisense or reverse control oligonucleotide was diluted to 2 μ M in OptiMEM™ and added to OptiMEM™ into which a delivery vehicle, preferably a lipitoid or cholesterol, had been diluted. The oligo/delivery vehicle mixture was then further diluted into medium with serum on the cells. The final concentration of oligonucleotide for all experiments was 300 nM, and
10 the final ratio of oligo to delivery vehicle for all experiments was 1.5 nmol lipitoid/ μ g oligonucleotide.

Antisense oligonucleotides were prepared. Cells were transfected for 4 hours or overnight at 37°C and the transfection mixture was replaced with fresh medium. Plates are incubated for 4 days, with a plate harvested for each day0-day4. To determine differences in
15 cell number, a CyQuant Cell Proliferation Assay kit (Molecular Probes) was used per manufacturer's instructions. Fluorecence readings (480nm excitation 520 nm emission) are taken after incubation for 5 minutes.

The results of these assays are shown in Tables 7A and 8. The data show that DKFZ antisense polynucleotides significantly reduce cell proliferation as compared to controls,
20 and, as such, DKFZ plays a role in production or maintenance of the cancerous phenotype in cancerous breast cells.

Table 7A:

Cell proliferation

Oligo	Cell Line	Ave Day0	Ave Day1	Ave Day2	Av3 Day3	Ave Day4
Untreated	MDA231	4233	4858	9544	10981	16776
Untreated	MDA231	3849	4036	8686	9855	14865
Pos Control	MDA231	3630	2236	3564	4536	7477
Neg Control	MDA231	4913	5127	8331	8887	13620
CHIR180-7AS	MDA231	3848	3476	6942	8715	11925
CHIR180-7RC	MDA231	4895	4700	8484	10318	14226
Untreated	T4-2	4062	3389	5438	10579	15617
Untreated	T4-2	4209	3802	6346	11802	16275
Pos Control	T4-2	3985	2712	4081	6404	9685
Neg Control	T4-2	4051	3901	4356	9425	12964
CHIR180-7AS	T4-2	3792	3201	3849	7376	10911
CHIR180-7RC	T4-2	3967	3840	4321	8382	12293

Table 8

Oligo	Standard Deviations					P-Value of T-Test				
	Day 0	Day 1	Day 2	Day 3	Day 4	Day0	Day1	Day2	Day3	Day4
Untreated	337	269	299	697	1333	0.1306	0.1063	0.1804	0.0926	0.1225
Untreated	99	631	867	547	1047	0.1306	0.1063	0.1804	0.0926	0.1225
Pos Control	94	118	89	441	974	0.0000	0.0001	0.0003	0.0001	0.0010
Neg Control	2	252	697	195	780	0.0000	0.0001	0.0003	0.0001	0.0010
CHIR180-7 AS	292	16	435	398	418	0.0072	0.0276	0.0059	0.0140	0.0028
CHIR180-7 RC	208	6	244	533	440	0.0072	0.0276	0.0059	0.0140	0.0028
Untreated	64	283	789	1593	1226	0.2550	0.0921	0.1257	0.2794	0.4352
Untreated	22	158	205	577	478	0.2550	0.0921	0.1257	0.2794	0.4352
Pos Control	122	213	6	475	957	0.4320	0.0065	0.2624	0.0051	0.0293
Neg Control	47	335	464	809	1417	0.4320	0.0065	0.2624	0.0051	0.0293
CHIR180-7 AS	170	679	263	127	1330	0.2638	0.0976	0.3516	0.0040	0.0039
CHIR180-7 RC	22	453	646	579	884	0.2638	0.0976	0.3516	0.0040	0.0039

EXAMPLE 10

5

ROLE OF DKFZ IN ANCHORAGE INDEPENDENT CELL GROWTH

The effect of DKFZ gene expression upon anchorage-independent cell growth of MDA435 and MCF7 human breast cancer cells was measured by colony formation in soft agar. Soft agar assays were conducted by the method described for GAK, above.

The data presented in Table 9 shows that the application of DKFZ antisense oligonucleotides to MDA435 and MCF7 cells results in inhibition of colony formation and shows that DKFZ plays a role in anchorage-independent cell growth of cancer cells. Table 9 shows the average fluorescence reading for several experiments. The standard deviation (St. Dev) of the fluorescence reading and coefficient of variation (%CV) and probability (P-value) is also shown.

Table 9

Oligo	Cell Line	Average	St. Dev	%CV	P-Value
Untreated	MDA435	31190	5838	19	0.1342
Untreated	MDA435	38623	3620	9	0.1342
Pos Control	MDA435	4776	818	17	0.0156
Neg Control	MDA435	16315	481	3	0.0156
Chir180-7AS	MDA435	21161	3439	16	0.0274
Chir180-7RC	MDA435	28868	1902	7	0.0274
Untreated	MCF7	18954	1478	8	0.1476
Untreated	MCF7	14383	4163	29	0.1476
Pos Control	MCF7	1036	194	19	0.0036
Neg Control	MCF7	9478	2382	25	0.0036
Chir180-7AS	MCF7	4752	2002	42	0.0139
Chir180-7RC	MCF7	9570	18	0	0.0139

The effect of DKFZ gene expression upon invasiveness of MDA231 human breast cancer cells was measured by a matrigel assay. A 3-dimensional reconstituted basement membrane culture of cells was generated as described previously (Peterson et al., (1992) *Proc. Natl. Acad. Sci. USA* 89:9064-9068) using a commercially prepared reconstituted basement membrane (Matrigel; Collaborative Research, Waltham, MA) and examined using methods well known in the art.

Table 10 (quantitated using Alamar Blue similar to the soft agar assay) and Figure 3 provides exemplary results of the Matrigel invasion/motility assay to test the invasiveness of

MDA231 cells with reduced expression of DKFZ. In general, these data show that a reduction in the expression of DKFZ significantly decreases the invasiveness of MDA231 cells.

Table 10:

Oligo	Cell Line	Average	St. Dev	%CV	P-Value
Untreated	MDA231	28316	13663	48	0.9080
Untreated	MDA231	26840	15669	58	0.9080
Pos Control	MDA231	2756	487	18	0.0002
Neg Control	MDA231	14301	1386	10	0.0002
Chir180-7AS	MDA231	10508	1963	19	0.0287
Chir180-7RC	MDA231	14310	153	1	0.0287

5

EXAMPLE 11

EXPRESSION OF DKFZ IN CANCER TISSUES

The following peptides were used for polyclonal antibody production: peptide 809: gvhqqyvqriek (SEQ ID NO:380), corresponding to amino acids 97-108 of the DKFZ protein and peptide 810: sgaepddeeyqef (SEQ ID NO:381), corresponding to amino acids 215-227 of the DKFZ protein.

10

Antibodies specific for DKFZ are used in FACS and immunolocalization analysis to show that DKFZ is associated with membrane, and up-regulated in cancer tissues of biopsies from cancer patients.

15

Further, antibodies specific for DKFZ are used to modulate DKFZ activity in cancerous breast, and is further used, alone or conjugated to a toxic moiety, as a treatment for breast cancer.

20

While the present invention has been described with reference to the specific embodiments thereof, it should be understood by those skilled in the art that various changes may be made and equivalents may be substituted without departing from the true spirit and scope of the invention. In addition, many modifications may be made to adapt a particular situation, material, composition of matter, process, process step or steps, to the objective, spirit and scope of the present invention. All such modifications are intended to be within the scope of the claims appended hereto

Table 1

SPOTID	SAMPLE ID	GENBANK NO	GENBANK DESCRIPTION	GENBANK SCORE
10594	I:1871362:05B01:A04	M62994	Homo sapiens thyroid autoantigen (truncated actin-binding protein) mRNA, complete cds	8.6E-36
21851	M00055153A:A12			
20990	I:1986550:13B02:G12	XM_005667	Homo sapiens lipocalin 2 (oncogene 24p3) (LCN2), mRNA	0
18641	I:3473302:09A01:A09	AB046098	Macaca fascicularis brain cDNA, clone:QccE-15843	5.8E-57
17229	I:1506962:09A01:G01	AL365454	Homo sapiens mRNA full length insert cDNA clone EUROIIMAGE 926491	2.6E-110
25930	035JN020.F01	AJ010446	Homo sapiens mRNA for immunoglobulin kappa light chain, anti-RhD, therad 24	0
20701	RG:730349:10010:G12	U28387	Human hexokinase II pseudogene, complete cds	0
20346	RG:1839794:10015:E11	U28387	Human hexokinase II pseudogene, complete cds	0
21247	M00054680C:A06	U28387	Human hexokinase II pseudogene, complete cds	9.9E-80
23062	M00056353C:E10	XM_011013	Homo sapiens filamin B, beta (actin-binding protein-278) (FLNB), mRNA	0
25666	035Jn031.B01	AF191633	Homo sapiens filamin (FLNB) gene, exon 48 and complete cds	0
19001	I:2171401:09A02:E09	AF123887	Homo sapiens ERO1L (ERO1L) mRNA, partial cds	3.3E-104
10897	I:1852047:02A01:A10	U22384	Human lysyl oxidase gene, partial cds	0
1960	M00023297B:A10	M33376	Human pseudo-chlordecone reductase mRNA, complete cds	0
26381	035JN029.H02	AB037838	Homo sapiens mRNA for KIAA1417 protein, partial cds	0
26719	035JN030.A02	X68277	H.sapiens CL 100 mRNA for protein tyrosine phosphatase	0
27152	037XN007.A09	XM_048479	Homo sapiens hypothetical protein FLJ14642 (FLJ14642), mRNA	7.3E-58
10926	I:2047770:08B02:G04	AK000969	Homo sapiens cDNA FLJ10107 fis, clone HEMBA1002583	3.8E-94
28980	035JN003.C12	XM_027456	Homo sapiens hypothetical gene supported by AK000584 (LOC89942), mRNA	0
1236	M00022024A:F02			
29350	035JN008.D06	XM_043864	Homo sapiens phosphoinositide-3-kinase, regulatory subunit, polypeptide 1 (p85 alpha) (PIK3R1), mRNA	0
26242	035JN015.B02	AL137717	Homo sapiens mRNA; cDNA DKFZp434J1630 (from clone DKFZp434J1630)	2.6E-70
4098	M00001439D:C09	BC002446	Homo sapiens, MRJ gene for a member of the DNAJ protein family, clone MGC:1152 IMAGE:3346070, mRNA, complete cds	0
17432	I:1965049:16B02:D07	XM_051165	Homo sapiens DKFZP586A0522 protein (DKFZP586A0522), mRNA	0
1785	SL198	XM_051165	Homo sapiens DKFZP586A0522 protein (DKFZP586A0522), mRNA	0
28856	035JN032.E11	X62996	H.sapiens mitochondrial genome (consensus sequence)	0
18791	RG:229957:10007:D03	D42042	Human mRNA for KIAA0085 gene, partial cds	0
22950	M00056922C:C09			
1882	M00022196B:D09	Z29083	H.sapiens 5T4 gene for 5T4 Oncofetal antigen	0
23886	M00055408A:F10			
24995	M00055215C:E11	XM_012880	Homo sapiens hypothetical protein MGC1936 (MGC1936), mRNA	0
24477	M00055510B:F08	AF240697	Homo sapiens retinol dehydrogenase homolog isoform-2 (RDH) mRNA, complete cds	0

Table 1

SPOTID	SAMPLE ID	GENBANK NO	GENBANK DESCRIPTION	GENBANK SCORE
21681	M00056771C:A12	X02152	Human mRNA for lactate dehydrogenase-A (LDH-A, EC 1.1.1.27)	0
9557	I:1335140:05A02:C08	X02152	Human mRNA for lactate dehydrogenase-A (LDH-A, EC 1.1.1.27)	0
22033	M00056574B:A07			
873	M00007979C:C05	X00663	Human mRNA fragment for epidermal growth factor (EGF) receptor	0
17144	RG:25254:10004:D07	M97675	Human transmembrane receptor (ror1) mRNA, complete cds	0
26970	035JN015.F09	AF097514	Homo sapiens stearoyl-CoA desaturase (SCD) mRNA, complete cds	0
21402	M00054507C:D07			
27074	035Jn031.B03	AF061741	Homo sapiens retinal short-chain dehydrogenase/reductase retSDR1 mRNA, complete cds	0
10963	I:1258790:05A02:B10	AF072752	Homo sapiens ten integrin EGF-like repeat domains protein precursor (ITGBL1) mRNA, complete cds	0
29525	035JN026.D12			
25514	035JN011.F01	U62961	Human succinyl CoA:3-oxoacid CoA transferase precursor (OXCT) mRNA, complete cds	0
26612	035JN016.C08	NM_000240	Homo sapiens monoamine oxidase A (MAOA), nuclear gene encoding mitochondrial protein, mRNA	0
24600	M00055490C:G11	U57059	Homo sapiens Apo-2 ligand mRNA, complete cds	0
9741	I:3126828:12A02:G02	U37518	Human TNF-related apoptosis inducing ligand TRAIL mRNA, complete cds	0
23689	M00054752A:E11	XM_001468	Homo sapiens S100 calcium-binding protein A10 (annexin II ligand, calpactin I, light polypeptide (p11)) (S100A10), mRNA	0
22352	M00042842B:E02	XM_001468	Homo sapiens S100 calcium-binding protein A10 (annexin II ligand, calpactin I, light polypeptide (p11)) (S100A10), mRNA	0
23806	RG:2007319:20003:G10			
12285	I:1404669:04A01:G12	BC002517	Homo sapiens, Pirin, clone MGC:2083 IMAGE:3140037, mRNA, complete cds	0
27638	035JN011.D10	AK002155	Homo sapiens cDNA FLJ11293 fis, clone PLACE1009670, highly similar to Homo sapiens genethonin 1 mRNA	0
9663	I:2488567:11A02:H08	XM_006027	Homo sapiens brain-derived neurotrophic factor (BDNF), mRNA	0
26850	035JN003.B03	XM_031551	Homo sapiens similar to carbohydrate (N-acetylglucosamine-6-O) sulfotransferase 2 (H. sapiens) (LOC90414), mRNA	0
10204	I:1491445:02B01:F09	AF131765	Homo sapiens clone 24833 nonsyndromic hearing impairment protein mRNA sequence, complete cds	0
1318	2192-6			
25922	035JN020.B01	AB020673	Homo sapiens mRNA for KIAA0866 protein, complete cds	0
26347	035JN025.G02			
20361	I:395116:17A02:E05			
28672	035JN012.A05	AF126181	Homo sapiens breast cancer-associated gene 1 protein (BCG1) mRNA, complete cds	0
25520	035JN011.A07	D86956	Human mRNA for KIAA0201 gene, complete cds	0
1723	M00005694A:A09	BC001980	Homo sapiens, clone IMAGE:3462291, mRNA	0

Table 1

SPOTID	SAMPLE ID	GENBANK NO	GENBANK DESCRIPTION	GENBANK SCORE
28863	037XN002.A05			
25526	035JN011.D07	AF086281	Homo sapiens full length insert cDNA clone ZD45G11	0
27936	035JN008.A04	X59445	H. sapiens mRNA for colon carcinoma Manganese Superoxide Dismutase	0
26851	035JN001.C03	XM_033944	Homo sapiens superoxide dismutase 2, mitochondrial (SOD2), mRNA	0
25107	M00054825A:E04	AF075061	Homo sapiens full length insert cDNA YP07G10	0
24912	M00054505D:D06	AF075061	Homo sapiens full length insert cDNA YP07G10	0
25169	M00055510D:D04	M11167	Human 28S ribosomal RNA gene	1.2E-76
25600	035JN023.A01	BC003107	Homo sapiens, inhibitor of DNA binding 3, dominant negative helix-loop-helix protein, clone MGC:1988 IMAGE:3543936, mRNA, complete	0
28706	035JN016.B05	X55181	Human ETS2 gene, 3'end	0
26377	035JN029.F02	Y14436	Homo sapiens mRNA for phosphatidic acid phosphatase type 2	0
19460	I:438655:14B02:B04	AF007133	Homo sapiens clone 23764 mRNA sequence	4.5E-113
25243	RG:1667183:10014:F12	BC000013	Homo sapiens, insulin-like growth factor binding protein 3, clone MGC:2305 IMAGE:3506666, mRNA, complete cds	0
20018	I:1213574:17B01:A11	AB037925	Homo sapiens MAIL mRNA, complete cds	3.7E-106
918	M00026895D:H03	BC006433	Homo sapiens, Ras-related GTP-binding protein, clone MGC:13077 IMAGE:3835186, mRNA, complete cds	0
25027	RG:1983823:20002:B06			
29089	035JN017.B06	XM_037534	Homo sapiens phosphodiesterase 7A (PDE7A), mRNA	0
9141	I:1347384:02A02:C07	U78579	Human type I phosphatidylinositol-4-phosphate 5-kinase beta (STM7) mRNA, partial cds	0
12005	I:1259230:05A01:C06	D87075	Human mRNA for KIAA0238 gene, partial cds	0
12148	I:3360476:03B01:B12	XM_040922	Homo sapiens interleukin 13 receptor, alpha 2 (IL13RA2), mRNA	0
17394	RG:1943755:10016:A07	AF346607	Homo sapiens interleukin-1 receptor associated kinase 1b (IRAK) mRNA, complete cds, alternatively spliced	0
27017	035JN021.F03	XM_051742	Homo sapiens spermine synthase (SMS), mRNA	0
25809	035JN002.B07	XM_009699	Homo sapiens nuclear receptor interacting protein 1 (NRIP1), mRNA	0
8719	I:2600080:10A01:H01	XM_009665	Homo sapiens Kreieler (mouse) maf-related leucine zipper homolog (KRML), mRNA	0
21030	RG:1714832:10015:C06	XM_029957	Homo sapiens Rab acceptor 1 (prenylated) (RABAC1), mRNA	0
11436	I:1470085:03B01:F05	XM_038976	Homo sapiens N-ethylmaleimide-sensitive factor attachment protein, alpha (NAPA), mRNA	0
10374	I:1513989:03B02:C03	XM_009010	Homo sapiens complement component 3 (C3), mRNA	1.4E-96
19037	I:417827:15A01:G10	X79538	H. sapiens nuk_34 mRNA for translation initiation factor	1.9E-28
398	M00027016A:C05	XM_031470	Homo sapiens aldolase C, fructose-bisphosphate (ALDOC), mRNA	4E-62
18773	I:1211682:14A02:C09	XM_008477	Homo sapiens aldolase C, fructose-bisphosphate (ALDOC), mRNA	0
3583	M00023407B:C10			
3418	M00001470A:C03	XM_043951	Homo sapiens CDP-diacylglycerol-inositol 3-phosphatidyltransferase (phosphatidylinositol synthase) (CDIPT), mRNA	0

Table 1

SPOTID	SAMPLE ID	GENBANK NO	GENBANK DESCRIPTION	GENBANK SCORE
18985	I:1402615:09A02:E03	AF191148	Homo sapiens type I transmembrane protein Fn14 mRNA, complete cds	7.9E-64
25861	035JN010.D01	XM_047975	Homo sapiens hydroxyacyl glutathione hydrolase (HAGH), mRNA	0
3317	M00003974D:E04	AF136185	Homo sapiens collagen type XVII (COL17A1) gene, 3' UTR, long form	0
8743	I:1858905:04A01:D01	U36775	Human ribonuclease 4 gene, partial cds	2.1E-57
26240	035JN015.A02	XM_007493	Homo sapiens ribonuclease, RNase A family, 4 (RNASE4), mRNA	0
28562	037XN007.B11	X00947	Human alpha 1-antichymotrypsin gene fragment	0
16877	I:2362945:15A01:C07	XM_029378	Homo sapiens checkpoint suppressor 1 (CHES1), mRNA	1.9E-91
25955	035JN022.C01	AF035620	Homo sapiens BRCA1-associated protein 2 (BRAP2) mRNA, complete cds	0
26308	035JN023.C02	XM_041470	Homo sapiens zinc finger protein 145 (Kruppel-like, expressed in promyelocytic leukemia) (ZNF145), mRNA	0
4140	2239-4	X03083	Human lactate dehydrogenase-A gene exon 7 and 3' flanking region	0
3436	2239-1	X03083	Human lactate dehydrogenase-A gene exon 7 and 3' flanking region	0
25612	035JN023.G01	M94856	Human fatty acid binding protein homologue (PA-FABP) mRNA, complete cds	0
12257	I:1448135:04A01:A06	X15535	H.sapiens lysosomal acid phosphatase gene (EC 3.1.3.2) Exon 11	0
9111	I:1958902:04A02:D07	D87258	Homo sapiens mRNA for serin protease with IGF-binding motif, complete cds	0
17620	I:875567:15B01:B08	XM_045326	Homo sapiens MAX-interacting protein 1 (MXI1), mRNA	0
26025	035JN030.F01	XM_032511	Homo sapiens procollagen-proline, 2-oxoglutarate 4-dioxygenase (proline 4-hydroxylase), alpha polypeptide I (P4HA1), mRNA	0
19271	RG:686684:10010:D04	AF005216	Homo sapiens receptor-associated tyrosine kinase (JAK2) mRNA, complete cds	0
4151	2035-1	D87953	Human mRNA for RTP, complete cds	0
26569	035JN010.F02	AB004788	Homo sapiens mRNA for BNIP3L, complete cds	0
10344	I:2859338:11B02:D03	XM_005052	Homo sapiens angiopoietin 1 (ANGPT1), mRNA	1.3E-97
832	M00021649B:D05	XM_004628	Homo sapiens hypoxia-inducible protein 2 (HIG2), mRNA	0
12071	I:1798283:06A01:D06	S72481	pantophysin [human, keratinocyte line HaCaT, mRNA, 2106 nt]	0
12271	I:1445767:04A01:H06	X12701	H.sapiens mRNA for endothelial plasminogen activator inhibitor PAI	1.8E-130
11433	I:1526282:03A01:E05	XM_033627	Homo sapiens glycoprotein (transmembrane) nmb (GPNMB), mRNA	3.7E-117
20917	RG:222350:10007:C12	X00663	Human mRNA fragment for epidermal growth factor (EGF) receptor	1.7E-122
25810	035JN004.B07	X00588	Human mRNA for precursor of epidermal growth factor receptor	0
12039	I:3506985:07A01:D06	M24795	Human CD36 antigen mRNA, complete cds	0
25499	035JN005.G07	XM_028224	Homo sapiens N-acetylglucosamine-phosphate mutase (AGM1), mRNA	0
25557	035JN013.D07	BC010135	Homo sapiens, cyclin C, clone IMAGE:4106819, mRNA	0
9917	I:1283532:05A01:G09	XM_004148	Homo sapiens 5T4 oncofetal trophoblast glycoprotein (5T4), mRNA	2.4E-70

Table 1

SPOTID	SAMPLE ID	GENBANK NO	GENBANK DESCRIPTION	GENBANK SCORE
19505	RG:204653:10007:A10	<u>XM_003789</u>	Homo sapiens colony stimulating factor 1 receptor, formerly McDonough feline sarcoma viral (v-fms) oncogene homolog (CSF1R), mRNA	0
17491	RG:277866:10008:B07	<u>XM_003789</u>	Homo sapiens colony stimulating factor 1 receptor, formerly McDonough feline sarcoma viral (v-fms) oncogene homolog (CSF1R), mRNA	0
10683	I:1686726:06A01:F10	<u>XM_003789</u>	Homo sapiens colony stimulating factor 1 receptor, formerly McDonough feline sarcoma viral (v-fms) oncogene homolog (CSF1R), mRNA	0
1936	M00008020C:H09	<u>X68277</u>	H.sapiens CL 100 mRNA for protein tyrosine phosphatase	0
828	M00021638B:F03	<u>X68277</u>	H.sapiens CL 100 mRNA for protein tyrosine phosphatase	0
9558	I:1824443:05B02:C08	<u>XM_003708</u>	Homo sapiens gamma-aminobutyric acid (GABA) A receptor, pi (GABRP), mRNA	0
20164	I:1997963:14B02:B05	<u>XM_003631</u>	Homo sapiens solute carrier family 25 (mitochondrial carrier, adenine nucleotide translocator), member 4 (SLC25A4), mRNA	0
969	NIH50_40026	<u>BC008664</u>	Homo sapiens, clone MGC:9281 IMAGE:3871960, mRNA, complete cds	0
9910	I:1805840:05B01:C09	<u>XM_003399</u>	Homo sapiens mannosidase, beta A, lysosomal (MANBA), mRNA	0
2427	M00005767D:B03	<u>XM_047441</u>	Homo sapiens RAP1, GTP-GDP dissociation stimulator 1 (RAP1GDS1), mRNA	0
19990	RG:1056692:10012:C11	<u>XM_003450</u>	Homo sapiens cyclin G associated kinase (GAK), mRNA	0
20605	I:690313:16A01:G12	<u>XM_011152</u>	Homo sapiens insulin-like growth factor binding protein 7 (IGFBP7), mRNA	0
10650	I:2456393:07B01:E10	<u>AK001580</u>	Homo sapiens cDNA FLJ10718 fis, clone NT2RP3001096, weakly similar to Rattus norvegicus leprecan mRNA	0
25963	035JN022.G01	<u>X53002</u>	Human mRNA for integrin beta-5 subunit	0
25562	035JN015.F07	<u>X53002</u>	Human mRNA for integrin beta-5 subunit	0
9377	I:2782593:12A01:A02	<u>X60656</u>	H.sapiens mRNA for elongation factor 1-beta	1.4E-46
17618	I:707667:15B01:A08	<u>XM_002273</u>	Homo sapiens inhibitor of DNA binding 2, dominant negative helix-loop-helix protein (ID2), mRNA	3.5E-117
12136	I:3208994:03B01:D06	<u>U16267</u>	Human AMP deaminase isoform L, alternatively spliced (AMPD2) mRNA, exons 1A, 2 and 3, partial cds	0
17373	I:1538189:14A02:G07	<u>XM_046818</u>	Homo sapiens similar to receptor tyrosine kinase-like orphan receptor 1 (H. sapiens) (LOC92711), mRNA	8.3E-123
18577	RG:503209:10010:A09	<u>XM_049305</u>	Homo sapiens Lysosomal-associated multispanning membrane protein-5 (LAPTM5), mRNA	0
3143	M00001605D:C02	<u>BC003107</u>	Homo sapiens, inhibitor of DNA binding 3, dominant negative helix-loop-helix protein, clone MGC:1988 IMAGE:3543936, mRNA, complete	1.7E-88
17737	RG:155066:10006:E02	<u>AL050147</u>	Homo sapiens mRNA; cDNA DKFZp586E0820 (from clone DKFZp586E0820); partial cds	0
20029	I:1923613:17A01:G11	<u>AF113123</u>	Homo sapiens carbonyl reductase mRNA, complete cds	0
18537	NIH50_40304	<u>BC001380</u>	Homo sapiens, succinate dehydrogenase complex, subunit A, flavoprotein (Fp), clone MGC:1484 IMAGE:3051442, mRNA, complete cds	0

Table 1

SPOTID	SAMPLE ID	GENBANK NO	GENBANK DESCRIPTION	GENBANK SCORE
10090	NIH50_40304			
12102	I:2832414:11B01:C06	XM_048045	Homo sapiens katanin p80 (WD40-containing) subunit B 1 (KATNB1), mRNA	0
8487	I:1375115:05A01:D01	BC001174	Homo sapiens, exostoses (multiple) 1, clone MGC:2129 IMAGE:3502232, mRNA, complete cds	0
9252	I:1673876:06B01:B02	BC000917	Homo sapiens, clone MGC:5184 IMAGE:3048750, mRNA, complete cds	0
25605	035JN021.D01	BC000671	Homo sapiens, claudin 4, clone MGC:1778 IMAGE:3349211, mRNA, complete cds	0
29652	M00001610C:D05	BC000588	Homo sapiens, HIRA-interacting protein 3, clone MGC:1814 IMAGE:3345739, mRNA, complete cds	0
10858	I:2458933:04B01:E04	X97544	H.sapiens mRNA for TIM17 preprotein translocase	8.7E-62
1261	M00023419C:B06	U89606	Human pyridoxal kinase mRNA, complete cds	0
4156	2243-4	X93334	Homo sapiens mitochondrial DNA, complete genome	0
3452	2243-1	X93334	Homo sapiens mitochondrial DNA, complete genome	0
2748	2242-6	X93334	Homo sapiens mitochondrial DNA, complete genome	0
2046	2248-3	X93334	Homo sapiens mitochondrial DNA, complete genome	0
2044	2242-4	X93334	Homo sapiens mitochondrial DNA, complete genome	0
1342	2248-2	X93334	Homo sapiens mitochondrial DNA, complete genome	0
1326	2244-3	X93334	Homo sapiens mitochondrial DNA, complete genome	0
9981	I:1720149:06A01:G09	AF069604	Homo sapiens myosin light chain kinase isoform 4 (MLCK) mRNA, partial cds	0
27917	035JN002.H04	XM_015978	Homo sapiens hypothetical protein FLJ22969 (FLJ22969), mRNA	1.8E-92
8488	I:1808529:05B01:D01	AJ293647	Homo sapiens partial IL4RA gene for interleukin-4 receptor alfa chain, exon 11, ECSSQV allele	1.1E-125
22793	M00057283C:D06	AF161410	Homo sapiens HSPC292 mRNA, partial cds	0
26883	035JN005.C03	AF161410	Homo sapiens HSPC292 mRNA, partial cds	0
11540	I:1909488:10B01:B11	XM_027739	Homo sapiens duodenal cytochrome b (FLJ23462), mRNA	0
17707	I:489882:14A01:F02	X99474	H.sapiens mRNA for chloride channel, CIC-6c	0
20649	NIH50_41452	Z14136	H.sapiens gene for spermidine/spermine N1-acetyltransferase	0
24004	M00056163C:H09	AF107495	Homo sapiens FWP001 and putative FWP002 mRNA, complete cds	0
11836	I:1806769:01B02:F11	X93036	H.sapiens mRNA for MAT8 protein	0
24932	M00054963C:C09	M26152	Homo sapiens serum amyloid A (SAA) mRNA, complete cds	0
19143	RG:149960:10006:D04	AK003448	Mus musculus 18 days embryo cDNA, RIKEN full-length enriched library, clone:1110004P15, full insert sequence	8.9E-21
26257	035JN013.B08	J04056	Human carbonyl reductase mRNA, complete cds	0
21239	M00054679B:B03	J02619	Human Z type alpha-1-antitrypsin gene, complete cds (exons 2-5)	0
16959	I:1426031:14B01:B07	AY035783	Homo sapiens laminin 5 beta 3 subunit (LAMB3) mRNA, complete cds	3.8E-121

Table 1

SPOTID	SAMPLE ID	GENBANK NO	GENBANK DESCRIPTION	GENBANK SCORE
2568	M00022158D:C11	<u>XM_036609</u>	Homo sapiens laminin, beta 3 (nicein (125kD), kalinin (140kD), BM600 (125kD)) (LAMB3), mRNA	0
25936	035JN020.A07	<u>XM_036608</u>	Homo sapiens laminin, beta 3 (nicein (125kD), kalinin (140kD), BM600 (125kD)) (LAMB3), mRNA	0
23041	M00054797C:G10	<u>XM_046649</u>	Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, alpha (NFKBIA), mRNA	0
9206	I:1822716:05B01:C08	<u>BC008059</u>	Homo sapiens, clone IMAGE:2967491, mRNA	0
25105	M00054824C:H04	<u>BC009110</u>	Homo sapiens, clone MGC:17355 IMAGE:3453825, mRNA, complete cds	0
24779	M00057061D:G07			
22451	M00043372B:B06	<u>X00947</u>	Human alpha 1-antichymotrypsin gene fragment	0
22291	M00054785D:G05	<u>X00947</u>	Human alpha 1-antichymotrypsin gene fragment	0
21143	M00055146A:D11			
24751	M00054676B:D07	<u>X03083</u>	Human lactate dehydrogenase-A gene exon 7 and 3' flanking region	0
24294	M00056163D:E01	<u>X03083</u>	Human lactate dehydrogenase-A gene exon 7 and 3' flanking region	9.4E-110
24006	M00056163D:E01	<u>X03083</u>	Human lactate dehydrogenase-A gene exon 7 and 3' flanking region	0
25678	035Jn031.H01	<u>AK001670</u>	Homo sapiens cDNA FLJ10808 fis, clone NT2RP4000879, weakly similar to UBIQUITIN-ACTIVATING ENZYME E1	4.9E-53
22027	M00056534C:E08	<u>XM_003512</u>	Homo sapiens amphiregulin (schwannoma-derived growth factor) (AREG), mRNA	0
29495	035JN022.E12	<u>D83761</u>	Homo sapiens mRNA for mother against dpp (Mad) related protein, complete cds	0
24577	M00056654B:G02	<u>XM_038306</u>	Homo sapiens dual specificity phosphatase 6 (DUSP6), mRNA	0
23527	M00055865C:D04			
17090	I:341491:13B01:A01	<u>BC004490</u>	Homo sapiens, v-fos FBJ murine osteosarcoma viral oncogene homolog, clone MGC:11074 IMAGE:3688670, mRNA, complete cds	3.8E-98
25137	M00057167A:C07			
23772	M00056360A:E07	<u>BC004490</u>	Homo sapiens, v-fos FBJ murine osteosarcoma viral oncogene homolog, clone MGC:11074 IMAGE:3688670, mRNA, complete cds	0
1659	M00001350B:D10	<u>BC004490</u>	Homo sapiens, v-fos FBJ murine osteosarcoma viral oncogene homolog, clone MGC:11074 IMAGE:3688670, mRNA, complete cds	0
8497	I:2170638:05A01:A07	<u>BC006169</u>	Homo sapiens, Similar to SH3-domain binding protein 5 (BTK-associated), clone MGC:13234 IMAGE:4025362, mRNA, complete cds	5.2E-125
25272	M00054621A:D09	<u>AF161435</u>	Homo sapiens HSPC317 mRNA, partial cds	0
21216	M00056194B:G06	<u>XM_002844</u>	Homo sapiens procollagen-lysine, 2-oxoglutarate 5-dioxygenase (lysine hydroxylase) 2 (PLOD2), mRNA	0
11939	I:2938757:02A02:B05	<u>D43767</u>	Human mRNA for chemokine, complete cds	0
9191	I:1421929:05A01:D02	<u>X63629</u>	H.sapiens mRNA for p cadherin	2.4E-90
3429	2024-3	<u>AF002697</u>	Homo sapiens E1B 19K/Bcl-2-binding protein Nip3 mRNA, nuclear gene encoding mitochondrial protein, complete cds	0
2725	2024-1	<u>AF002697</u>	Homo sapiens E1B 19K/Bcl-2-binding protein Nip3 mRNA, nuclear gene encoding mitochondrial protein, complete cds	0

Table 1

SPOTID	SAMPLE ID	GENBANK NO	GENBANK DESCRIPTION	GENBANK SCORE
19923	I:1001356:13A01:B11	<u>BC006318</u>	Homo sapiens, erythrocyte membrane protein band 4.9 (dematin), clone MGC:12740 IMAGE:4125804, mRNA, complete cds	1.7E-103
20457	I:1923289:19A01:E06	<u>XM_035603</u>	Homo sapiens gap junction protein, beta 5 (connexin 31.1) (GJB5), mRNA	0
24773	M00057055D:B11			
24119	M00042886D:H10	<u>BC006260</u>	Homo sapiens, Similar to N-myc downstream regulated, clone MGC:11293 IMAGE:3946764, mRNA, complete cds	4.4E-114
3908	M00027080A:E06	<u>M60756</u>	Human histone H2B.1 mRNA, 3' end	0
8560	I:2346704:06B01:H01	<u>AJ000334</u>	Homo sapiens mRNA for cytosolic asparaginyl-tRNA synthetase	0
24588	M00055411A:C10	<u>L19779</u>	Homo sapiens histone H2A.2 mRNA, complete cds	0
4047	M00007997C:B08	<u>XM_009091</u>	Homo sapiens glycogen synthase 1 (muscle) (GYS1), mRNA	0
28344	035JN011.E11	<u>XM_050471</u>	Homo sapiens glycogen synthase 1 (muscle) (GYS1), mRNA	0
27561	035JN001.F04	<u>XM_001472</u>	Homo sapiens v-jun avian sarcoma virus 17 oncogene homolog (JUN), mRNA	0
3272	M00022165C:E12	<u>NM_001024</u>	Homo sapiens ribosomal protein S21 (RPS21), mRNA	0
26735	035JN030.A08	<u>XM_010408</u>	Homo sapiens RAB9-like protein (RAB9L), mRNA	0
24900	M00054500D:C08	<u>BC004427</u>	Homo sapiens, proteasome (prosome, macropain) subunit, alpha type, 7, clone MGC:3755 IMAGE:2819923, mRNA, complete cds	0
9472	I:2510171:04B01:H08	<u>X04503</u>	Human SLPI mRNA fragment for secretory leucocyte protease inhibitor	0
9979	I:1623318:06A01:F09	<u>L31409</u>	Homo sapiens creatine transporter mRNA, complete cds	2.2E-45
21996	M00042467B:B04	<u>L00160</u>	Human phosphoglycerate kinase (pgk) mRNA, exons 2 to last	0
22312	M00055035D:F05			
11327	I:3139773:05A01:H11	<u>L00160</u>	Human phosphoglycerate kinase (pgk) mRNA, exons 2 to last	2.6E-21
18240	RG:1927470:10015:H08	<u>V00572</u>	Human mRNA encoding phosphoglycerate kinase	0
21922	M00054848A:D12	<u>AF139065</u>	Homo sapiens desmoplakin I mRNA, partial cds	0
22290	M00057002D:H01			
10390	I:1405391:03B02:C09	<u>AF056979</u>	Homo sapiens clone YAN1 interferon-gamma receptor mRNA, complete cds	0
2212	M00008098B:F06	<u>U19247</u>	Homo sapiens interferon-gamma receptor alpha chain gene, exon 7 and complete cds	0
20213	RG:221172:10007:C11	<u>S74774</u>	p59fyn(T)=OKT3-induced calcium influx regulator [human, Jurkat J6 T cell line, mRNA Partial, 1605 nt]	2.9E-103
24955	M00055929D:D04			
19574	I:635178:13B02:C10	<u>XM_033944</u>	Homo sapiens superoxide dismutase 2, mitochondrial (SOD2), mRNA	0
19969	RG:501476:10010:A05	<u>U14394</u>	Human tissue inhibitor of metalloproteinases-3 mRNA, complete cds	0
8570	I:1696224:06B01:E07	<u>X70684</u>	C.aethiops mRNA for heat shock protein 70	5.6E-25
18519	I:1997703:13A01:D09	<u>X52947</u>	Human mRNA for cardiac gap junction protein	0
9616	I:3200341:06B02:H02	<u>Y00106</u>	Human gene for beta-adrenergic receptor (beta-2 subtype)	0

Table 1

SPOTID	SAMPLE ID	GENBANK NO	GENBANK DESCRIPTION	GENBANK SCORE
22334	M00055067D:H12			
17459	I:2056395:13A02:B07	M77349	Human transforming growth factor-beta induced gene product (BIGH3) mRNA, complete cds	2.5E-121
25193	M00056763B:A12	X68277	H.sapiens CL 100 mRNA for protein tyrosine phosphatase	0
25191	M00056763B:A12	X68277	H.sapiens CL 100 mRNA for protein tyrosine phosphatase	0
9448	I:2455617:04B01:D02	XM_051799	Homo sapiens guanosine monophosphate reductase (GMPR), mRNA	0
25224	RG:950682:10003:D06	BC002536	Homo sapiens, phosphofructokinase, platelet, clone MGC:2192 IMAGE:3140233, mRNA, complete cds	0
20218	RG:2158297:10016:E11	BC002536	Homo sapiens, phosphofructokinase, platelet, clone MGC:2192 IMAGE:3140233, mRNA, complete cds	0
3089	NIH50_26184	D25328	Human mRNA for platelet-type phosphofructokinase, complete cds	2E-108
23985	NIH50_26184			
19953	NIH50_26184	D25328	Human mRNA for platelet-type phosphofructokinase, complete cds	2E-108
11506	NIH50_26184			
22362	M00056349A:F08	M10546	Human mitochondrial DNA, fragment M1, encoding transfer RNAs, cytochrome oxidase I, and 2 URFs	1.2E-86
25516	035JN011.G01	XM_011470	Homo sapiens myristoylated alanine-rich protein kinase C substrate (MARCKS, 80K-L) (MACS), mRNA	0
25757	037XN005.H07	AF017116	Homo sapiens type-2 phosphatidic acid phosphohydrolase (PAP2) mRNA, complete cds	0
24814	M00042773B:E09	M17733	Human thymosin beta-4 mRNA, complete cds	0
21994	M00042465B:E04	M17733	Human thymosin beta-4 mRNA, complete cds	0
27117	037XN001.H03	BC001631	Homo sapiens, prothymosin beta 4, clone MGC:2219 IMAGE:3536637, mRNA, complete cds	0
24681	NIH50_41452			
22745	M00056592A:B08	NM_003739	Homo sapiens aldo-keto reductase family 1, member C3 (3-alpha hydroxysteroid dehydrogenase, type II) (AKR1C3), mRNA	0
24233	M00055873C:B06			
2001	M00001381A:F03	XM_035387	Homo sapiens ribosomal protein, large, P1 (RPLP1), mRNA	0
21179	NIH50_43550			
17147	NIH50_43550	AK026515	Homo sapiens cDNA: FLJ22862 fis, clone KAT01966, highly similar to HSLDHAR Human mRNA for lactate dehydrogenase-A	0
8700	NIH50_43550			
21214	M00056193B:D06	BC006260	Homo sapiens, Similar to N-myc downstream regulated, clone MGC:11293 IMAGE:3946764, mRNA, complete cds	0
26422	037XN003.D08	BC006260	Homo sapiens, Similar to N-myc downstream regulated, clone MGC:11293 IMAGE:3946764, mRNA, complete cds	0
22837	M00055891C:B09			
21965	M00057029A:G09			
25541	035JN013.D01	AK026310	Homo sapiens cDNA: FLJ22657 fis, clone HSI07791, highly similar to HUMCYB5 Human cytochrome b5 mRNA	0

Table 1

SPOTID	SAMPLE ID	GENBANK NO	GENBANK DESCRIPTION	GENBANK SCORE
18302	I:1738248:09B02:G08	XM_016114	Homo sapiens hypothetical protein FLJ22501 (FLJ22501), mRNA	0
24049	M00054706B:G04	AF107495	Homo sapiens FWP001 and putative FWP002 mRNA, complete cds	0
26326	035JN023.D08	AK025906	Homo sapiens cDNA: FLJ22253 fis, clone HRC02763	0
2254	M00004085C:C02	AK025703	Homo sapiens cDNA: FLJ22050 fis, clone HEP09454	0
10296	I:2868216:07B02:D09	AK025703	Homo sapiens cDNA: FLJ22050 fis, clone HEP09454	0
20044	I:2547084:09B01:F05	XM_016847	Homo sapiens hypothetical protein FLJ22002 (FLJ22002), mRNA	0
28806	035JN028.D05	AK025504	Homo sapiens cDNA: FLJ21851 fis, clone HEP01962	0
17566	I:446969:17B02:G07	AK023217	Homo sapiens cDNA FLJ13155 fis, clone NT2RP3003433	2E-115
19005	I:2674167:09A02:G09	AK022968	Homo sapiens cDNA FLJ12906 fis, clone NT2RP2004373	0
3567	M00023369D:C05			
21983	M00057081B:H03			
458	M00022134B:E08	XM_037412	Homo sapiens hypothetical gene supported by BC008993 (LOC91283), mRNA	0
22331	M00057138A:E11			
21411	M00055833D:B03			
22972	M00056956D:B01			
24533	RG:1643392:10014:C11			
24853	M00056617D:F07	AK020869	Mus musculus adult retina cDNA, RIKEN full-length enriched library, clone:A930017A02, full insert sequence	6.5E-59
23753	M00054915A:G02			
21502	M00056193B:D06			
18180	RG:39422:10005:B02			
23918	M00056278C:E03			
24144	RG:1982961:20001:H05			
19996	RG:1283072:10012:F11	BC009107	Homo sapiens, clone MGC:17352 IMAGE:3449913, mRNA, complete cds	0
11528	I:1899534:10B01:D05			
20506	I:1969044:18B01:E12	AB048286	Homo sapiens GS1999full mRNA, complete cds	0
23833	RG:1656861:10014:E10			
20042	I:1873176:09B01:E05	BC001909	Homo sapiens, clone IMAGE:3537447, mRNA, partial cds	0
24977	M00055820D:F01			
11646	I:1723142:08B02:G11	AK014612	Mus musculus 0 day neonate skin cDNA, RIKEN full-length enriched library, clone:4633401105, full insert sequence	4.6E-45
24872	RG:773612:10011:D06			
10577	I:2174196:08A01:A10			
21710	RG:1091554:10003:G01			
18556	RG:31082:10004:F09			
29433	035JN014.F12	AK001805	Homo sapiens cDNA FLJ10943 fis, clone OVARC1001360	0
29273	037XN005.F12			
28763	035JN018.G11	AJ310543	Homo sapiens mRNA for EGLN1 protein	1.9E-40
27887	RG:2364147:8119908:A10			
27450	035JN032.F09			
27255	035JN006.E09	XM_027456	Homo sapiens hypothetical gene supported by AK000584 (LOC89942), mRNA	1.2E-57

Table 1

SPOTID	SAMPLE ID	GENBANK NO	GENBANK DESCRIPTION	GENBANK SCORE
27226	035JN004.F09			
26550	035JN008.D08			
26508	035JN004.G02			
26483	RG:2377371:8119908:C08			
26334	035JN023.H08	AF364547	Homo sapiens methylmalonyl-CoA epimerase mRNA, complete cds; nuclear gene for mitochondrial product	0
26027	035JN030.G01			
25977	035JN022.F07			
25965	035JN022.H01			
25844	035JN008.C07			
25834	035JN008.F01	AB048289	Bos taurus lae mRNA for lipoate-activating enzyme, complete cds	3.1E-35
25816	035JN004.E07			
25746	037XN007.B07			
25742	037XN007.H01			
25741	037XN005.H01			
25712	037XN003.A07			
25642	035JN027.F01			
25621	035JN021.D07	AK027321	Homo sapiens cDNA FLJ14415 fis, clone HEMBA1004889, weakly similar to Human C3f mRNA	0
25614	035JN023.H01			
25603	035JN021.C01			
25556	035JN015.C07			
25555	035JN013.C07			
25540	035JN015.C01			
23576	RG:1984769:20002:D10			
22566	RG:1996656:20003:C03			
9036	DD182			
4164	M00007932B:E06			
4146	2179-5			
4091	M00026845A:E01			
4072	M00023398A:G12			
4022	M00022127D:B06			
3965	M00005406A:F04			
3954	M00005400B:E1			
3872	M00007974D:B04			
3869	M00003868C:A03			
3838	M00007052A:C09	XM_048272	Homo sapiens similar to Ras-related GTP-binding protein (H. sapiens) (LOC92951), mRNA	0
3806	2168-2			
3798	2138-4			
3792	2171-5			
3788	2156-4			
3767	M00001355D:H12			
3458	M00007160D:E10			
3251	M00005471A:a04			
3194	DF821			
3102	2167-1			
3094	2138-3			
2671	M00023431A:D02			
2634	M00008025D:A04			
2567	M00008061B:A12			
2317	M00001502D:E09			
1958	M00023296B:B09			
1680	2169-5			

Table 1

SPOTID	SAMPLE ID	GENBANK NO	GENBANK DESCRIPTION	GENBANK SCORE
1625	M00001542C:G08			
1445	M00023335C:C09			
1320	2207-5			
974	2161-1			
726	DO15			
718	ER418			
703	M00004189D:A11			
652	M00007070A:C08			
630	2203-2			
593	M00001373A:A06	<u>X93036</u>	H.sapiens mRNA for MAT8 protein	0
532	M00022005A:H05			
272	2168-5			
256	M00001406C:H12			
57	M00023371B:H02			

Table 2

SEQ ID NO.	SPOT ID	2D T4-2/ 2D S1	3D T4-2/ 3D S1	3D S1/ 2D S1	3D T4-2/ 2D T4-2	3D T4-2/ EGFR Ab	3D T4-2/ B1 Integrin Ab	3D T4-2/ Tyr
1	10594	0.6	2.2	0.6	1.9	3.0	1.0	2.9
2	21851	1.0	1.0	1.0	3.5	1.3	1.0	1.0
3	20990	1.6	4.6	1.0	1.5	1.0	1.0	1.0
4	18641	1.0	0.6	2.6	1.7	1.0	1.6	1.0
5	17229	0.3	0.8	1.0	2.1	1.0	1.0	1.0
6	25930	1.0	1.0	1.0	1.0	1.0	1.0	1.0
7	20701	1.6	2.9	1.3	2.7	4.5	1.9	5.8
8	20346	1.7	2.7	1.4	2.6	4.3	2.0	5.2
9	21247	1.0	4.4	1.5	3.0	3.4	2.6	4.7
10	23062	0.6	2.5	0.6	1.8	3.3	1.4	2.7
11	25666	1.0	2.9	0.6	2.0	3.6	1.0	2.3
12	19001	8.5	14.2	1.0	1.0	4.8	1.7	8.0
13	10897	1.0	3.1	4.5	1000.0	13.3	4.6	18.4
14	1960	0.3	1.5	3.0	13.7	3.9	2.4	4.9
15	26381	1.0	1.0	1.0	0.9	1.0	1.0	1.0
16	26719	0.4	1.0	0.6	2.8	1.2	1.7	1.0
17	27152	4.2	3.0	2.2	1.5	1.3	1.0	1.3
18	10926	0.7	1.9	0.9	2.1	3.7	1.5	3.3
19	28980	0.6	1.4	1.0	2.4	1.0	1.0	1.0
20	1236	1.0	2.8	0.8	2.1	2.2	1.8	3.2
21	29350	0.5	0.6	1.2	2.1	1.4	1.0	1.0
22	26242	1.0	1.0	0.6	2.2	1.0	1.0	2.0
23	4098	1.4	3.9	0.6	2.1	2.7	1.3	3.1
24	17432	0.4	0.3	2.4	2.1	0.3	0.9	0.3
25	1785	0.5	0.4	2.4	2.0	0.3	1.0	0.3
26	28856	8.5	0.9	2.5	0.3	0.6	1.0	0.5
27	18791	1.0	0.2	0.3	4.1	1.0	1.0	1.3
28	22950	3.9	4.1	1.2	1.0	2.1	1.0	2.4
29	1882	2.4	4.1	0.9	1.8	3.2	1.5	4.7
30	23886	1.0	1.0	1.2	2.1	1.0	1.0	1.0
31	24995	2.0	1.6	2.1	1.0	1.0	1.0	1.0
32	24477	1.0	1.9	1.0	4.2	2.7	1.3	1.8
33	21681	1.7	7.1	0.6	2.0	2.8	1.0	3.6
34	9557	1.6	7.5	0.8	1.0	3.0	1.0	2.5
35	22033	2.8	3.7	1.0	0.9	2.2	1.0	2.7
36	873	1.0	4.0	1.0	2.7	1.7	1.0	1.0
37	17144	1.0	0.5	3.6	1.4	1.0	1.0	1.0
38	26970	6.0	15.3	0.2	0.6	2.9	1.0	5.4
39	21402	0.2	1.0	2.8	6.9	2.4	1.0	3.6
40	27074	1.7	2.5	2.3	3.2	1.6	1.0	2.0
41	10963	0.5	0.3	2.1	0.5	1.0	1.0	0.7
42	29525	0.6	1.0	0.7	2.4	1.7	1.3	1.0
43	25514	1000.0	1.0	1.0	1.0	0.5	1.0	1.0
44	26612	0.4	0.5	1.6	2.8	0.8	1.0	0.8
45	24600	1.6	2.7	1.0	2.0	1.0	1.2	1.4
46	9741	2.3	5.0	1.0	2.2	1.7	1.0	1.0
47	23689	1.0	2.6	0.8	1.8	2.3	1.0	2.7
48	22352	1.0	2.9	0.7	1.6	2.4	1.0	2.4
49	23806	1.0	0.4	1.3	2.3	1.0	1.4	1.4
50	12285	1.0	1.0	1.0	1.0	0.8	1.0	0.5
51	27638	0.6	1.0	0.8	2.2	2.1	1.0	1.0
52	9663	1.0	1.0	1.0	1000.0	1.0	1.0	1.0
53	26850	1.0	0.2	9.1	2.1	1.3	1.6	2.2

Table 2

SEQ ID NO.	SPOT ID	2D T4-2/ 2D S1	3D T4-2/ 3D S1	3D S1/ 2D S1	3D T4-2/ 2D T4-2	3D T4-2/ EGFR Ab	3D T4-2/ B1 Integrin Ab	3D T4-2/ Tyr
54	10204	2.9	2.3	0.8	0.6	3.1	1.4	2.4
55	1318	2.0	0.9	2.3	0.5	0.6	1.1	0.7
56	25922	1.0	0.8	1.0	1.0	1.0	1.0	1.0
57	26347	1.0	1.0	1.0	1.0	1.0	1.0	1.0
58	20361	1.0	1.0	1.0	2.0	1.0	1.0	1.0
59	28672	0.6	2.1	0.6	2.1	1.4	1.0	1.7
60	25520	0.5	0.3	2.3	1.3	1.0	0.7	0.5
61	1723	1.0	0.5	5.1	3.5	1.0	3.1	1.0
62	28863	0.8	1.3	1.0	2.3	1.7	1.7	1.7
63	25526	5.9	1.7	1.0	0.6	0.6	0.7	0.4
64	27936	1.0	1.0	3.2	3.1	1.9	3.1	1.5
65	26851	1.0	0.7	3.2	2.7	1.6	2.4	1.3
66	25107	1.0	5.8	1.0	2.6	2.6	1.6	2.6
67	24912	1.0	2.9	1.0	2.4	1.6	1.3	1.8
68	25169	1.0	0.7	2.5	1.5	1.0	1.0	1.0
69	25600	1.6	1.4	2.9	2.1	0.7	0.9	0.5
70	28706	0.2	0.5	0.6	2.1	1.3	1.2	1.0
71	26377	0.6	0.3	2.2	1.0	1.2	1.3	1.0
72	19460	2.4	1.5	2.5	1.3	1.0	1.0	0.8
73	25243	1.0	0.7	2.2	1.0	1.0	1.0	1.0
74	20018	1.0	1.0	1.0	2.6	1.0	1.0	1.0
75	918	1.0	1.7	1.3	2.1	2.0	1.6	2.4
76	25027	1.0	1.0	1.0	1.0	1.0	1.0	1.0
77	29089	0.6	0.5	0.8	2.1	1.0	1.0	1.0
78	9141	1.0	1.0	1.0	1.0	1.0	1.0	1.0
79	12005	1.0	1.0	2.2	1.0	1.0	1.0	1.0
80	12148	1.0	1.0	1.0	1.0	1.0	1.0	1.0
81	17394	0.4	0.6	2.1	2.0	1.0	1.0	1.0
82	27017	2.8	3.3	0.8	1.0	2.4	1.8	2.8
83	25809	1.0	1.0	1000.0	1.0	1.0	1.0	1.0
84	8719	0.1	1.0	2.3	2.1	0.4	0.5	0.3
85	21030	0.4	1.0	1.3	2.1	1.4	1.6	1.4
86	11436	0.7	0.4	2.0	1.0	0.6	0.8	0.6
87	10374	1.5	1.5	3.5	2.7	0.4	1.0	0.3
88	19037	3.0	3.3	0.9	1.5	2.7	1.4	3.7
89	398	1.6	6.9	1.1	3.3	2.4	1.0	4.5
90	18773	1.9	5.1	1.0	3.9	3.8	2.0	6.1
91	3583	0.5	0.7	1.0	2.0	2.5	1.0	1.5
92	3418	1.8	3.2	1.2	2.4	1.6	1.0	1.2
93	18985	9.2	3.1	1.0	0.6	2.3	1.1	2.5
94	25861	3.4	1.5	2.0	0.8	0.8	0.9	0.6
95	3317	0.9	2.3	1.0	3.4	1.9	1.0	1.0
96	8743	0.2	0.7	1.0	4.3	1.8	1.0	1.7
97	26240	0.2	1.0	1.0	5.3	1.9	1.9	1.1
98	28562	0.3	0.2	2.0	1.0	0.5	0.5	0.6
99	16877	1.0	2.6	1.1	2.6	1.7	1.5	1.3
100	25955	1.0	1.0	1.0	1.0	1.0	1.0	1.0
101	26308	0.2	0.4	1.0	2.2	0.7	0.8	0.6
102	4140	1.9	6.7	0.7	2.1	3.0	1.0	3.5
103	3436	1.8	6.3	0.6	2.2	3.1	1.3	3.3
104	25612	1.0	12.5	1.0	1.0	2.1	1.0	2.9
105	12257	1.0	1.0	2.0	1.0	0.8	0.9	0.8
106	9111	0.5	0.5	2.2	1.3	1.5	1.0	0.7

Table 2

SEQ ID NO.	SPOT ID	2D T4-2/ 2D S1	3D T4-2/ 3D S1	3D S1/ 2D S1	3D T4-2/ 2D T4-2	3D T4-2/ EGFR Ab	3D T4-2/ B1 Integrin Ab	3D T4-2/ Tyr
107	17620	0.3	0.8	1.0	3.2	2.7	2.1	1.0
108	26025	1.0	2.9	1.1	2.2	2.3	1.0	2.6
109	19271	0.5	1.3	0.7	2.2	1.6	1.2	1.5
110	4151	0.4	4.2	1.2	11.1	4.2	1.0	2.9
111	26569	0.7	2.2	0.8	2.9	2.3	1.7	2.6
112	10344	1.0	1.0	1.0	1.0	1.0	1.0	1.0
113	832	1.0	3.3	1.0	2.4	3.7	2.2	4.0
114	12071	1.8	1.5	2.2	1.0	1.3	0.8	1.4
115	12271	0.6	4.9	1.9	14.9	20.8	4.0	24.1
116	11433	0.5	0.4	5.7	3.0	1.7	1.8	1.0
117	20917	1.0	2.8	0.9	2.6	1.7	1.4	1.7
118	25810	1.1	3.8	1.0	2.9	1.5	1.3	1.5
119	12039	1.0	1.0	3.6	1.0	1.0	1.0	1.0
120	25499	1.0	1.0	1.0	1.0	1.0	1.0	1.0
121	25557	1.0	1.8	1.0	0.8	1.0	1.0	1.0
122	9917	2.5	2.7	0.7	1.6	3.8	1.2	3.6
123	19505	0.4	1.7	0.7	3.8	1.7	1.6	1.4
124	17491	0.6	1.7	0.7	2.5	1.6	1.3	1.4
125	10683	0.4	1.9	0.6	3.6	1.7	1.4	1.1
126	1936	0.2	0.6	0.6	3.1	1.0	1.8	1.0
127	828	0.1	1.0	0.5	3.0	1.0	1.7	1.2
128	9558	1.0	1.0	1.0	1.0	1.0	1.0	1.0
129	20164	2.0	1.1	2.5	1.7	1.0	1.0	0.8
130	969	1.0	1.0	2.7	1.0	1.0	1.5	0.7
131	9910	0.4	1.0	0.8	3.2	1.9	1.3	1.4
132	2427	1.3	0.7	3.0	2.8	0.8	1.9	1.0
133	19990	1.0	7.9	2.8	34.7	1.0	1.0	1.0
134	20605	3.0	1.2	2.1	1.0	1.3	1.2	0.8
135	10650	0.5	1.7	0.5	2.9	2.8	0.6	3.4
136	25963	2.6	3.5	0.7	1.0	3.3	1.0	2.3
137	25562	3.2	5.9	0.7	1.0	4.2	1.0	4.8
138	9377	0.6	1.0	1.0	2.1	1.9	2.0	1.6
139	17618	1.0	0.7	2.3	3.2	0.8	0.7	0.8
140	12136	1.0	1.0	3.8	1.0	1.0	1.0	1.0
141	17373	1.0	0.4	6.1	2.4	1.0	1.0	1.0
142	18577	1.0	0.3	0.3	4.6	1.0	1.0	1.0
143	3143	1.7	1.3	2.6	2.3	0.7	1.0	0.5
144	17737	6.1	0.7	3.4	0.3	0.5	1.3	0.4
145	20029	1.0	0.6	2.3	1.0	1.0	1.0	0.5
146	18537	1.0	1.3	2.1	2.6	1.3	1.0	1.2
147	10090	1.0	1.7	2.1	2.8	1.5	1.0	1.2
148	12102	1.0	1.0	3.9	1.0	1.0	1.0	1.0
149	8487	4.7	2.4	1.0	1.0	2.3	1.1	2.2
150	9252	1.3	3.8	0.3	1.0	2.1	1.6	2.5
151	25605	1.0	1.0	1.0	1.0	0.5	0.5	1.0
152	29652	1.0	2.9	1.5	2.9	2.0	1.5	2.1
153	10858	1.0	0.8	2.0	1.0	1.0	1.0	0.7
154	1261	0.2	0.6	1.0	2.9	0.8	0.8	0.9
155	4156	12.4	0.8	3.1	0.2	0.6	1.0	0.3
156	3452	10.6	0.8	2.8	0.3	0.6	1.0	0.4
157	2748	10.8	0.8	3.1	0.2	0.5	1.0	0.4
158	2046	9.2	1.0	2.4	0.3	0.5	1.2	0.4
159	2044	11.7	0.8	2.8	0.2	0.6	1.4	0.4

Table 2

SEQ ID NO.	SPOT ID	2D T4-2/ 2D S1	3D T4-2/ 3D S1	3D S1/ 2D S1	3D T4-2/ 2D T4-2	3D T4-2/ EGFR Ab	3D T4-2/ B1 Integrin Ab	3D T4-2/ Tyr
160	1342	10.5	0.9	2.8	0.2	0.5	1.2	0.4
161	1326	12.2	1.0	2.7	0.2	0.5	1.0	0.4
162	9981	0.2	1.5	0.3	2.5	1.2	1.6	0.5
163	27917	1.9	2.5	0.5	1.0	2.1	1.4	2.3
164	8488	4.3	2.4	1.0	0.5	2.9	0.9	3.6
165	22793	1.9	2.6	0.5	1.0	2.2	1.8	2.1
166	26883	2.4	3.7	0.5	1.0	2.5	2.0	2.0
167	11540	0.7	1.0	1.3	2.8	0.8	1.0	0.5
168	17707	1.0	0.6	2.6	1.0	1.0	1.0	1.0
169	20649	2.3	2.6	0.5	0.4	3.0	1.0	3.1
170	24004	1.0	2.5	1.8	3.6	2.3	1.0	2.8
171	11836	1.2	5.0	0.9	3.7	1.3	1.0	0.8
172	24932	1.8	0.8	6.5	2.1	0.8	1.0	0.5
173	19143	0.6	1.6	0.7	2.0	1.7	1.2	1.4
174	26257	1.9	1.3	2.2	1.7	0.7	1.0	0.6
175	21239	9.4	9.2	0.5	0.4	2.4	1.0	2.7
176	16959	0.6	2.1	0.8	2.1	3.0	1.4	2.5
177	2568	0.7	1.9	0.7	2.2	3.0	1.3	2.4
178	25936	1.0	2.4	0.7	2.0	3.1	1.5	2.4
179	23041	0.7	1.0	2.1	2.6	1.0	1.4	1.0
180	9206	5.7	1.8	4.6	1.0	1.0	0.7	0.9
181	25105	1.6	1.3	2.1	1.0	1.0	0.7	0.8
182	24779	1.0	1.0	1.0	2.9	2.3	1.4	1.2
183	22451	1.0	0.2	2.1	1.0	1.4	0.6	1.0
184	22291	0.2	0.2	2.1	1.0	0.6	0.6	0.5
185	21143	1.0	7.2	0.7	2.0	2.6	1.1	2.4
186	24751	1.7	5.0	0.7	2.1	2.4	1.3	4.0
187	24294	1.7	3.9	0.8	2.4	2.6	1.1	3.9
188	24006	1.7	6.3	0.8	2.5	2.4	1.0	4.0
189	25678	1.0	1.0	1.0	1.0	1.0	1.0	1.0
190	22027	8.7	7.0	0.4	0.2	5.1	2.0	5.2
191	29495	1.0	1.0	1.0	1.0	1.0	1.0	1.0
192	24577	6.8	3.2	0.8	0.4	3.8	1.3	2.1
193	23527	0.3	2.1	1.6	6.4	2.7	2.1	3.4
194	17090	1.0	4.9	0.7	2.3	3.1	2.3	3.6
195	25137	1.0	1.0	0.4	3.8	1.0	2.5	4.1
196	23772	0.6	6.8	0.5	3.7	12.6	3.6	9.2
197	1659	1.0	7.5	0.3	3.2	17.8	4.1	20.3
198	8497	1.3	0.4	2.2	0.5	1.0	1.0	1.0
199	25272	8.0	6.0	1.0	0.6	2.2	1.0	2.9
200	21216	1.0	1.0	0.6	2.0	2.5	2.0	2.2
201	11939	1.0	1.0	1.0	1.0	1.0	1.0	1.0
202	9191	1.8	2.2	1.3	1.1	2.2	1.0	2.0
203	3429	0.7	3.4	0.8	3.5	3.0	1.5	3.7
204	2725	0.8	3.4	1.0	3.4	2.6	1.6	4.1
205	19923	1.0	1.1	2.9	1.0	1.7	1.4	1.2
206	20457	1.0	2.0	1.0	2.3	2.9	1.0	2.3
207	24773	0.2	1.0	0.8	2.0	1.6	1.0	1.0
208	24119	0.2	4.6	1.1	15.9	2.7	1.0	3.4
209	3908	0.3	0.5	1.1	2.3	1.7	1.0	1.0
210	8560	1.9	0.7	2.2	0.5	1.0	1.0	0.7
211	24588	0.3	0.5	1.0	2.0	1.0	1.0	1.4
212	4047	0.5	1.2	1.0	2.1	1.9	1.0	1.8

Table 2

SEQ ID NO.	SPOT ID	2D T4-2/ 2D S1	3D T4-2/ 3D S1	3D S1/ 2D S1	3D T4-2/ 2D T4-2	3D T4-2/ EGFR Ab	3D T4-2/ B1 Integrin Ab	3D T4-2/ Tyr
213	28344	0.8	1.0	1.0	2.0	1.7	1.5	2.7
214	27561	1.0	1.0	1.0	2.4	1.2	1.2	1.3
215	3272	0.6	0.8	1.0	2.1	1.3	1.6	1.0
216	26735	1.0	1.0	1.0	1.0	1.0	1.0	1.0
217	24900	0.3	0.8	2.9	5.7	2.2	1.1	3.0
218	9472	2.2	5.0	1.0	2.0	1.5	0.8	1.7
219	9979	1.3	3.3	1.5	3.9	3.4	1.4	2.5
220	21996	1.0	4.7	1.0	3.4	2.5	1.0	2.4
221	22312	1.2	4.4	1.2	3.3	2.2	1.1	2.2
222	11327	1.4	6.2	1.4	2.7	2.7	1.0	2.2
223	18240	2.0	4.5	1.0	2.2	2.1	1.0	2.7
224	21922	0.7	1.4	0.8	2.1	1.8	1.0	1.3
225	22290	0.7	1.6	0.9	2.1	1.5	1.2	1.3
226	10390	1.3	1.0	2.6	1.6	0.8	1.0	0.6
227	2212	1.9	1.0	2.8	1.0	0.6	1.6	0.8
228	20213	0.4	1.0	1.0	1.0	1.0	1.0	1.0
229	24955	0.9	2.9	1.0	3.3	0.8	0.8	1.0
230	19574	1.0	0.6	3.7	3.1	1.5	2.6	1.4
231	19969	1.0	1.0	1.0	3.1	1.0	1.0	1.0
232	8570	0.4	1.2	1.0	2.6	1.2	0.8	0.6
233	18519	3.5	2.9	2.6	1.8	1.8	1.0	2.0
234	9616	0.6	2.0	1.0	2.3	1.2	1.2	1.0
235	22334	0.2	0.7	2.9	8.5	1.7	1.1	3.4
236	17459	0.1	0.7	2.7	18.8	4.0	1.3	4.6
237	25193	1.0	0.8	1.0	2.3	1.0	1.3	1.0
238	25191	0.2	0.8	0.7	2.5	1.3	1.5	1.2
239	9448	0.6	1.0	1.0	2.3	0.8	0.8	0.5
240	25224	5.6	14.4	1.0	2.3	6.0	1.5	9.6
241	20218	6.1	12.3	0.7	1.7	5.6	1.6	9.0
242	3089	7.0	15.7	0.7	2.3	7.3	1.8	8.0
243	23985	5.8	17.2	0.9	2.1	6.8	1.8	8.1
244	19953	6.2	13.5	0.8	1.8	6.4	1.7	10.4
245	11506	4.1	13.3	1.0	1.4	4.4	1.6	7.2
246	22362	1.0	0.7	4.1	2.1	1.2	1.8	1.0
247	25516	0.7	10.1	0.4	4.0	14.7	4.7	8.1
248	25757	0.6	0.4	2.4	1.0	1.0	1.3	0.9
249	24814	0.5	2.8	0.3	1.0	3.5	1.4	4.4
250	21994	0.5	3.2	0.3	1.0	3.6	1.0	4.3
251	27117	1.0	2.8	0.3	1.0	3.9	1.0	4.9
252	24681	1.8	2.6	0.6	0.5	3.2	1.5	3.0
253	22745	0.3	2.4	1.4	8.1	2.8	2.3	3.5
254	24233	1.9	3.9	1.3	2.3	1.3	0.8	2.2
255	2001	1.0	1.0	1.5	2.1	1.0	1.0	1.0
256	21179	2.0	7.9	0.7	1.9	2.1	1.0	4.3
257	17147	1.3	4.3	0.7	1.7	2.4	1.2	3.9
258	8700	1.5	7.3	0.7	1.6	3.1	1.0	2.7
259	21214	0.3	5.4	1.2	15.5	3.1	1.0	3.6
260	26422	0.4	3.7	1.0	12.7	3.9	1.0	3.3
261	22837	0.7	1.0	2.1	2.4	1.2	1.5	0.9
262	21965	1.0	1.0	1.0	2.2	2.4	1.0	1.0
263	25541	4.5	2.7	2.7	0.8	1.0	1.3	0.8
264	18302	1.1	0.9	2.1	1.0	1.0	1.0	1.0
265	24049	1.0	2.6	1.5	2.5	2.3	1.4	2.4

Table 2

SEQ ID NO.	SPOT ID	2D T4-2/ 2D S1	3D T4-2/ 3D S1	3D S1/ 2D S1	3D T4-2/ 2D T4-2	3D T4-2/ EGFR Ab	3D T4-2/ B1 Integrin Ab	3D T4-2/ Tyr
266	26326	9.2	1.5	3.2	0.7	0.7	0.9	1.0
267	2254	1.6	3.3	1.0	2.8	2.0	1.1	3.1
268	10296	0.9	1.7	2.9	5.0	2.1	1.0	1.3
269	20044	1.0	0.8	2.0	1.0	1.0	1.0	1.0
270	28806	2.8	1.1	2.1	1.0	0.9	1.2	0.8
271	17566	7.5	4.2	0.7	0.5	2.5	1.0	2.5
272	19005	1.0	0.8	1.0	2.1	1.0	1.0	1.0
273	3567	1.0	1.0	1.0	1.0	1.0	1.0	1.0
274	21983	0.1	1.0	3.1	25.6	3.4	1.0	4.7
275	458	1.0	2.1	0.6	1.0	1.6	2.1	2.3
276	22331	0.6	2.1	0.4	1.0	2.2	1.0	2.8
277	21411	0.7	1.5	1.0	2.5	1.0	1.0	1.0
278	22972	1.0	2.2	0.5	1.0	2.2	1.4	2.4
279	24533	1.0	2.5	1.0	2.0	2.0	2.7	3.2
280	24853	1.0	2.6	2.1	2.1	2.4	1.3	2.1
281	23753	0.7	1.5	1.3	2.1	2.0	1.7	2.3
282	21502	0.3	4.8	1.0	10.8	2.6	1.0	2.9
283	18180	0.3	0.8	0.8	2.4	0.9	1.4	0.7
284	23918	0.7	2.3	0.4	1.0	2.4	1.2	3.5
285	24144	1.0	1.0	1.0	1.0	1.0	1.6	1.0
286	19996	1.5	2.5	0.7	1.2	2.1	0.9	2.5
287	11528	1.0	1.0	1.0	2.1	1.0	1.0	1.0
288	20506	2.2	0.9	3.2	0.8	1.3	1.6	1.0
289	23833	1.0	0.5	2.1	1.0	1.0	1.0	0.7
290	20042	3.8	1.6	2.3	0.8	1.0	1.0	1.0
291	24977	1.0	1.0	2.1	1.0	2.3	1.4	1.4
292	11646	1.0	1.0	0.8	1000.0	1.0	1.0	1.7
293	24872	1.0	1.4	0.8	2.5	1.4	1.2	1.3
294	10577	1.0	1.0	1.0	1.0	1.0	1.0	1.0
295	21710	1.0	0.2	2.2	0.7	1.6	1.0	1.2
296	18556	0.0	1.0	1.0	1.0	1.0	1.0	1.0
297	29433	1.0	0.5	1.0	2.1	1.0	1.0	1.0
298	29273	1.0	2.2	1.0	2.2	1.0	1.3	1.0
299	28763	1.6	2.7	1.0	2.2	1.8	1.3	2.5
300	27887	0.1	0.2	1.1	2.7	0.8	1.0	0.6
301	27450	2.6	11.3	0.2	1.0	4.4	3.3	7.3
302	27255	0.6	1.6	0.8	2.3	1.7	1.4	1.5
303	27226	1.0	1.3	1.0	2.6	1.8	1.0	1.0
304	26550	4.2	17.9	0.2	1.0	6.9	2.9	9.2
305	26508	1.0	1.4	1.0	1.0	1.0	1.0	1.0
306	26483	1.2	2.2	0.6	1.0	2.1	1.4	2.7
307	26334	1.0	0.5	3.0	1.0	0.6	0.8	0.5
308	26027	1.0	1.0	1.0	1.5	1.0	1.0	1.0
309	25977	1.0	1.0	1.0	1.0	1.0	1.0	1.0
310	25965	1.0	1.0	1.0	1.0	1.0	1.0	1.0
311	25844	1.0	1.0	1.0	1.0	1.0	1.0	1.0
312	25834	1000.0	1.0	1.0	1.0	0.4	1.0	1.0
313	25816	1.0	1.0	1.0	1.0	1.0	1.0	1.0
314	25746	1.0	1.0	1.0	1.0	1.0	1.0	1.0
315	25742	1.0	1.0	1.0	1.0	0.5	1.0	1.0
316	25741	1.0	1.0	1.0	1.0	1.0	1.0	1.0
317	25712	1.0	1.0	1.0	1.0	1.0	1.0	1.0
318	25642	1.0	1.0	1.0	1.0	1.0	1.0	1.0

Table 2

SEQ ID NO.	SPOT ID	2D T4-2/ 2D S1	3D T4-2/ 3D S1	3D S1/ 2D S1	3D T4-2/ 2D T4-2	3D T4-2/ EGFR Ab	3D T4-2/ B1 Integrin Ab	3D T4-2/ Tyr
319	25621	0.6	0.8	2.1	2.0	1.3	1.2	1.0
320	25614	1.0	1.0	1.0	1.0	1.0	1.0	1.0
321	25603	1.0	1.0	1.0	1.0	1.0	1.0	1.0
322	25556	1.8	0.7	1.0	0.8	1.0	1.0	1.0
323	25555	1.0	2.9	1.0	1.0	1.5	1.3	1.0
324	25540	1.0	1.0	1.0	1.2	1.0	1.0	1.0
325	23576	0.0	1.0	1.0	1.0	1.0	1.5	1.4
326	22566	1.0	1.0	1.0	1.0	1.0	1.3	1.0
327	9036	1.9	3.8	0.6	1.8	2.6	1.3	3.1
328	4164	1.0	1.0	2.2	1.0	1.5	1.0	0.9
329	4146	0.8	3.7	0.9	4.4	3.3	1.0	4.3
330	4091	1.0	1.0	1.0	2.5	1.7	1.0	0.9
331	4072	1.0	1.0	2.1	1.0	5.9	2.0	5.1
332	4022	3.5	4.5	0.8	1.0	3.0	1.0	3.2
333	3965	1.9	5.6	0.4	1.0	5.5	2.3	4.1
334	3954	1.0	2.7	1.3	3.6	2.8	1.9	2.6
335	3872	1.0	3.2	1.3	2.8	4.0	1.8	3.9
336	3869	1.0	1.0	5.8	3.8	1.0	0.7	0.6
337	3838	1.0	1.6	1.2	2.0	2.6	1.7	1.9
338	3806	0.6	2.6	0.9	3.7	3.0	1.0	3.4
339	3798	10.2	0.9	2.9	0.3	0.7	1.0	0.4
340	3792	1.0	1.0	1.0	2.7	2.9	1.0	2.5
341	3788	1.7	5.4	1.2	3.4	2.5	1.3	2.7
342	3767	1.1	2.2	0.7	1.7	2.5	1.0	2.5
343	3458	1.2	3.3	0.7	2.0	2.6	1.0	2.2
344	3251	0.4	0.5	1.4	2.7	1.4	1.0	1.0
345	3194	1.0	2.3	1.3	3.1	2.2	1.3	3.2
346	3102	0.5	3.2	1.0	4.8	2.9	1.0	2.3
347	3094	11.5	0.8	2.7	0.3	0.6	1.0	0.4
348	2671	0.8	1.6	1.0	2.2	2.8	1.9	1.0
349	2634	0.9	2.8	0.4	1.0	3.8	1.7	4.0
350	2567	4.6	3.3	0.8	0.6	2.6	1.0	3.3
351	2317	1.0	1.0	2.4	1.0	1.0	1.0	1.1
352	1958	0.3	0.6	1.0	2.6	0.9	0.8	0.9
353	1680	0.3	4.7	1.0	17.7	2.7	1.0	4.5
354	1625	2.2	7.8	0.5	1.8	3.1	1.7	3.4
355	1445	0.2	0.6	1.0	2.7	0.8	0.9	0.9
356	1320	4.9	1.0	2.4	0.4	0.6	1.2	0.5
357	974	0.6	3.1	1.1	3.2	2.4	1.4	3.7
358	726	1.0	1.0	1.0	1.0	1.0	1.0	1.0
359	718	0.4	2.6	0.5	2.7	1.6	1.0	1.0
360	703	1.0	4.1	1.0	2.4	1.6	1.0	1.7
361	652	2.8	4.4	1.6	2.3	1.0	1.6	1.0
362	630	6.9	1.0	2.2	0.3	0.6	1.0	0.5
363	593	1.0	4.3	1.0	2.3	1.0	1.0	1.0
364	532	1.3	4.7	1.0	2.4	2.6	2.2	4.0
365	272	0.7	2.7	0.9	3.1	2.4	1.3	4.3
366	256	0.6	3.2	0.5	1.9	2.8	1.0	3.4
367	57	0.5	1.4	1.0	2.3	0.9	1.0	0.7

Table 11

SEQ ID NO	SPOT ID
1	10594
2	21851
3	20990
4	18641
5	19037
6	398
7	18773
8	3583
9	3418
10	145306
11	3418
12	3418
13	18985
14	17229
15	25930
16	25930
17	20701
18	20346
19	20346
20	21247
21	21247
22	23062
23	25666
24	25666
25	19001
26	10897
27	10897
28	10897
29	1960
30	146262
31	26381
32	26381
33	26719
34	26719
35	27152
36	10926
37	28980
38	1236
39	29350
40	29350

Table 11

SEQ ID NO	SPOT ID
41	26242
42	4098
43	145253
44	4098
45	17432
46	17432
47	1785
48	1785
49	1785
50	28856
51	28856
52	18791
53	18791
54	22950
55	22950
56	1882
57	23886
58	24995
59	24995
60	24477
61	21681
62	21681
63	9557
64	9557
65	22033
66	873
67	17144
68	26970
69	26970
70	21402
71	27074
72	27074
73	10963
74	10963
75	29525
76	29525
77	25514
78	25514
79	26612
80	26612

Table 11

SEQ ID NO	SPOT ID
81	24600
82	9741
83	9741
84	9741
85	23689
86	23689
87	22352
88	23806
89	12285
90	27638
91	27638
92	9663
93	9663
94	26850
95	10204
96	10204
97	10204
98	25922
99	25922
100	26347
101	26347
102	20361
103	20361
104	28672
105	28672
106	25520
107	25520
108	1723
109	1723
110	28863
111	25526
112	25526
113	27936
114	27936
115	26851
116	25107
117	25107
118	25107
119	24912
120	24912

Table 11

SEQ ID NO	SPOT ID
121	25169
122	25600
123	25600
124	28706
125	28706
126	26377
127	26377
128	19460
129	25243
130	20018
131	20018
132	918
133	25027
134	29089
135	29089
136	9141
137	9141
138	9141
139	12005
140	12148
141	12148
142	17394
143	27017
144	27017
145	25809
146	8719
147	8719
148	21030
149	21030
150	11436
151	11436
152	10374
153	10374
154	25861
155	25861
156	3317
157	3317
158	8743
159	26240
160	26240

Table 11

SEQ ID NO	SPOT ID
161	28562
162	16877
163	25955
164	26308
165	26308
166	4140
167	3436
168	25612
169	25612
170	12257
171	12257
172	9111
173	9111
174	17620
175	26025
176	26025
177	19271
178	4151
179	4151
180	26569
181	26569
182	10344
183	10344
184	10344
185	832
186	832
187	12071
188	12071
189	12271
190	11433
191	20917
192	25810
193	12039
194	12039
195	25499
196	25499
197	25557
198	25557
199	9917
200	19505

Table 11

SEQ ID NO	SPOT ID
201	17491
202	10683
203	10683
204	1936
205	828
206	9558
207	9558
208	20164
209	969
210	969
211	9910
212	2427
213	19990
214	20605
215	20605
216	10650
217	10650
218	25963
219	25963
220	25562
221	25562
222	3429
223	2725
224	19923
225	20457
226	20457
227	24773
228	24119
229	3908
230	3908
231	8560
232	8560
233	9377
234	9377
235	17618
236	12136
237	17373
238	18577
239	18577
240	3143

Table 11

SEQ ID NO	SPOT ID
241	17737
242	17737
243	20029
244	20029
245	18537
246	18537
247	12102
248	12102
249	8487
250	9252
251	9252
252	25605
253	25605
254	29652
255	10858
256	1261
257	4156
258	4156
259	3452
260	3452
261	2748
262	2046
263	2046
264	2044
265	2044
266	1342
267	1342
268	1326
269	1326
270	9981
271	9981
272	27917
273	8488
274	22793
275	22793
276	26883
277	26883
278	11540
279	17707
280	20649

Table 11

SEQ ID NO	SPOT ID
281	20649
282	24004
283	24004
284	11836
285	11836
286	11836
287	24932
288	19143
289	19143
290	26257
291	26257
292	21239
293	21239
294	16959
295	2568
296	25936
297	25936
298	23041
299	9206
300	25105
301	25105
302	24779
303	22451
304	22451
305	22291
306	22291
307	21143
308	24751
309	24751
310	24294
311	24294
312	24006
313	24006
314	25678
315	25678
316	22027
317	29495
318	29495
319	24577
320	24577

Table 11

SEQ ID NO	SPOT ID
321	24577
322	23527
323	17090
324	25137
325	23772
326	1659
327	8497
328	25272
329	21216
330	21216
331	21216
332	11939
333	11939
334	11939
335	9191
336	3429
337	24588
338	4047
339	28344
340	28344
341	27561
342	3272
343	26735
344	26735
345	24900
346	24900
347	9472
348	9472
349	9979
350	21996
351	22312
352	11327
353	18240
354	18240
355	21922
356	21922
357	22290
358	10390
359	10390
360	2212

Table 11

SEQ ID NO	SPOT ID
361	20213
362	20213
363	24955
364	19574
365	19969
366	8570
367	18519
368	9616
369	9616
370	17459
371	17459
372	25193
373	25193
374	25193
375	25191
376	22566
377	4164
378	4146
379	4072
380	4022
381	3954
382	3838
383	3806
384	3798
385	3792
386	3788
387	3458
388	3194
389	3102
390	25191
391	25191
392	9448
393	9448
394	25224
395	20218
396	3089
397	3089
398	19953
399	19953
400	22362

Table 11

SEQ ID NO	SPOT ID
401	25516
402	25516
403	25757
404	24814
405	21994
406	27117
407	22745
408	24233
409	2001
410	2001
411	2001
412	17147
413	21214
414	21214
415	21214
416	26422
417	21965
418	25541
419	25541
420	18302
421	18302
422	24049
423	24049
424	26326
425	26326
426	2254
427	162502
428	10296
429	20044
430	28806
431	17566
432	17566
433	19005
434	3567
435	159223
436	3567
437	3567
438	458
439	21411
440	22972

Table 11

SEQ ID NO	SPOT ID
441	24853
442	21502
443	18180
444	23918
445	24144
446	19996
447	11528
448	20506
449	20506
450	23833
451	20042
452	20042
453	11646
454	10577
455	10577
456	18556
457	29433
458	28763
459	27450
460	27450
461	27255
462	26550
463	26550
464	26508
465	26334
466	26334
467	26027
468	26027
469	25977
470	25977
471	25965
472	25965
473	25844
474	25844
475	25834
476	25816
477	25746
478	25712
479	25621
480	25621

Table 11

SEQ ID NO	SPOT ID
481	25614
482	25614
483	25603
484	25603
485	25556
486	25556
487	25555
488	25555
489	3094
490	2567
491	1958
492	1680
493	1445
494	1320
495	974
496	652
497	630
498	593
499	256